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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:58:47 ; Search time 75.59 Seconds
(without alignments)
17.633 Million cell updates/sec

Title: US-09-884-696-6

Perfect score: 57
Sequence: 1 FLSLNKELEAE 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	57	100.0	927	22	AA862110	M. bovis Dalton 26
	2	43	75.4	450	22	AAE04637	Pasteurella haemol
	3	43	75.4	608	22	AAE04636	Pasteurella haemol
	4	43	75.4	924	12	AA810889	leukotoxin 352 enc
	5	43	75.4	924	14	AA842385	Recombinant leukot
	6	43	75.4	924	14	AA842380	Recombinant leukot
	7	43	75.4	924	14	AA842378	Recombinant leukot
	8	43	75.4	926	12	AA814482	LKT352. Pasteurel
	9	43	75.4	926	14	AA834545	leukotoxin 352 pro
	10	43	75.4	926	15	AA850291	Recombinant leukot
	11	43	75.4	926	17	AAW03945	P. haemolytica trit

12	43	75.4	926	19	AAM75567	Leukotoxin 352 pol
13	43	75.4	936	14	AAR34547	GnRH-Leukotoxin ge
14	43	75.4	943	14	AAR34546	Somatostatin-Leuko
15	43	75.4	951	11	AAR34548	Rotavirus VP4-Leuk
16	43	75.4	953	11	AAR07167	105kD PRX protein
17	43	75.4	953	12	AAR15159	Leukotoxin from P.
18	43	75.4	953	14	AAR34865	Leukotoxin protein f
19	43	75.4	953	15	AAR60072	PpxA protein of Pa
20	43	75.4	953	22	AAE04638	Pasteurella haemo
21	43	75.4	956	12	AAR12561	APPA haemolysin an
22	43	75.4	956	18	AAW22156	Apjitic protein. A
23	43	75.4	956	21	AAV51410	A. pleuropneumonia
24	43	75.4	977	17	AAW03942	LKT-GnRH protein f
25	43	75.4	977	19	AAW79569	LKT-GnRH chimeric
26	43	75.4	1069	15	AAK52748	Bovine IFNgamma/LK
27	43	75.4	1069	18	AAW13867	Chimeric protein #
28	43	75.4	1069	21	AAAB21074	Bovine gamma-IFN/B
29	43	75.4	1098	13	AAAR22103	Bovine IL-2 - LKT
30	43	75.4	1098	15	AAAR52747	Bovine IL-2/LKT ch
31	43	75.4	1098	18	AAAI3866	Chimeric protein #
32	43	75.4	1098	21	AAAB21073	Bovine IL-2/Pasteu
33	43	75.4	1098	21	AAAY31518	Extendin agonist pe
34	41	71.9	28	20	AAV24822	Extendin agonist pe
35	41	71.9	28	20	AAV17577	Extendin agonist pe
36	41	71.9	28	21	AAAB11444	extendin agonist pe
37	41	71.9	28	21	AAAB11234	extendin agonist pe
38	41	71.9	28	21	AAAB52903	Extendin agonist p
39	41	71.9	28	21	AAAB53007	Extendin agonist c
40	41	71.9	28	21	AAV94057	Amino acid sequenc
41	41	71.9	28	21	AAV94155	Amino acid sequen
42	41	71.9	28	22	AAAE08396	Extendin agonist pe
43	41	71.9	28	22	AAE08486	Extendin agonist pe
44	41	71.9	28	22	AAAB64232	Extendin agonist,
45	41	71.9	28	22	AAAB64322	Extendin agonist,

ALIGNMENTS

RESULT	1	
ID	AAAB62110	standard; Protein; 927 AA.
XX	AAAB62110:	
AC	AAAB62110:	
XX	29-MAY-2001	(first entry)
DE	M. bovis Dalton 2d RTX toxin A subunt.	
XX		
KM	Moraxella; antigen: Immune response; Infection; RTX toxin; vaccine;	
KW	antibacterial; A subunit.	
XX		
OS	Moraxella bovis.	
XX		
PN	WO200116172-A1.	
XX		
PD	08-MAR-2001.	
XX		
PF	31-AUG-2000; 2000MO-AU01048.	
XX		
PR	31-AUG-1999; 99AU-0002571.	
XX		
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.	
PA	(UYME) UNIV MELBOURNE.	
PI	Farn J, Strugnelli R, Tennent J;	
XX		
DR	WPI; 2001-235092/24.	
XX		
DR	N-PSDB; AAF57290.	
PT	Novel Moraxella bovis antigen useful in compositions for raising immune	
XX	response in an animal, has protease, lipase or hemolysin activity -	
XX		

PS Claim 26; Fig 5; 60pp; English.

XX The invention relates to new Moraxella bovis antigens and nucleic acid
CC sequences encoding these antigenic polypeptides. The antigenic
CC polypeptides and polynucleotides are useful for raising an immune
CC response in an animal directed against Moraxella, preferably against
CC M. bovis or M. catarrhalis, and for treating Moraxella infections. The
CC present sequence represents the amino acid sequence of the A subunit of
CC the RTX toxin from M. bovis Dalton 2d.

SQ Sequence 927 AA;

Query Match 100.0%; Score 57; DB 22; Length 927;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
DB 433 flselnkelgae 444

RESULT 2

AAE04637
ID AAE04637 standard; Protein: 450 AA.

AC AAE04637;

DT 10-SEP-2001 (first entry)

DE Pasteurella haemolytica modified leukotoxin 50 (Lkt50) protein.

KW Leukotoxin 50; Lkt50; respiratory disease; infection; therapy;

KW Immunostimulant; antibacterial; vaccine; transgenic plant;

KW animal feed; mutant; mutain.

OS Pasteurella haemolytica.

OS Synthetic.

PN WO200144289-A2.

PD 21-JUN-2001.

PF 15-DEC-2000; 2000WO-CA01498.

PR 17-DEC-1999; 99US-0172148.

PT (UYGU-) UNIV GUELPH OFFICE.

PI Lo RYC, Shewen PE, Lee RWH, Hodgins D, Strommer JN;

DR WPI: 2001-408470/43.

DR N-PSDB: AAD08976.

XX Modified leukotoxin polypeptide is useful in a vaccine to prevent or
PT treat Mannheimia (Pasteurella) infection (particularly M. haemolytica
PT infection), and disease associated with a leukotoxin, e.g., respiratory
PT disease -

PS Claim 4; Fig 12; 70pp; English.

XX The present sequence is Pasteurella (Mannheimia) haemolytica

CC modified leukotoxin-50 (Lkt50) protein. The modification comprises

CC the removal of amino acids within the hydrophobic transmembrane

CC domain of a full length leukotoxin protein. Modified leukotoxin

CC sequences are used in vaccines to treat or prevent diseases associated

CC with leukotoxin, e.g., respiratory disease, and Mannheimia infection
CC (particularly M. haemolytica infection). In addition, the vaccine
CC is used to prepare a medicament. Furthermore, the plant transformed
CC with modified leukotoxin sequences is fed to an animal such as a
CC ruminant, to prevent or treat respiratory diseases.

SQ Sequence 450 AA;

Query Match 75.4%; Score 43; DB 22; Length 450;

Best Local Similarity 75.0%; Pred. No. 23;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
DB 1 flinlnkelgae 12

RESULT 3

AAE04636
ID AAE04636 standard; Protein: 608 AA.

AC AAE04636;

DT 10-SEP-2001 (first entry)

DE Pasteurella haemolytica modified leukotoxin 66 (Lkt66) protein.

KW Leukotoxin 66; Lkt66; respiratory disease; infection; therapy;

KW Immunostimulant; antibacterial; vaccine; transgenic plant;

KW animal feed; mutant; mutain.

OS Pasteurella haemolytica.

OS Synthetic.

PN WO200144289-A2.

PD 21-JUN-2001.

PF 15-DEC-2000; 2000WO-CA01498.

PR 17-DEC-1999; 99US-0172148.

PT (UYGU-) UNIV GUELPH OFFICE.

PI Lo RYC, Shewen PE, Lee RWH, Hodgins D, Strommer JN;

DR WPI: 2001-408470/43.

DR N-PSDB: AAD08975.

XX Modified leukotoxin polypeptide is useful in a vaccine to prevent or
PT treat Mannheimia (Pasteurella) infection (particularly M. haemolytica
PT infection), and disease associated with a leukotoxin, e.g., respiratory
PT disease -

PS Claim 2; Fig 2; 70pp; English.

XX The present sequence is Pasteurella (Mannheimia) haemolytica

CC modified leukotoxin-66 (Lkt66) protein. The modification comprises

CC the removal of amino acids within the hydrophobic transmembrane

CC domain of a full length leukotoxin protein. Modified leukotoxin

CC sequences are used in vaccines to treat or prevent diseases associated

CC with leukotoxin, e.g., respiratory disease, and Mannheimia infection
CC (particularly M. haemolytica infection). In addition, the vaccine
CC is used to prepare a medicament. Furthermore, the plant transformed
CC with modified leukotoxin sequences is fed to an animal such as a
CC ruminant, to prevent or treat respiratory diseases.

SQ Sequence 608 AA;

Query Match 75.4%; Score 43; DB 22; Length 608;

Best Local Similarity 75.0%; Pred. No. 33;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
DB 106 flinlnkelgae 117

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RESULT 4
AAR10889
ID AAR10889 standard; Protein: 924 AA.
XX
AC AAR10889;
XX
DT 11-APR-1991 (first entry)
XX
DE Leukotoxin 352 encoded by plasmid pAA352.
XX
KM LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia.
XX
OS Pasteurella haemolytica A1 strain B122.
XX
PN CA2014033-A.
XX
PD 07-OCT-1990.
XX
PF 06-APR-1990; 90CA-2014033.
XX
PR 07-APR-1989; 89US-0335018.
XX
PA (UYSA-) UNIV SASKATCHEWAN.
XX
PI Acres SD, Babluk LA, Potter AA, Lawman MJP;
XX
DR WPI; 1991-000097/01.
DR N-PSDB; AAQ10272.
XX
PT Pasteurella haemolytica proteins and genes - used for producing
PT vaccines to protect animals esp. cattle from respiratory diseases
PT e.g. pneumonia.
XX
PS Claim 13; Fig 5; 87pp; English.
XX
CC Plasmid pAA352 is derived from pAA114, a clone isolated from a
CC genomic library of P. haemolytica. The protein, designated "new
CC leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin.
CC LKT 352 and pref. antigenic fragments of it, can be used in
CC vaccines to protect cattle from respiratory diseases. They can also
CC be used to produce antibodies for immunoinfinity purification.
CC further proteins. [Fig. contg. sequence v. poor].
CC See also AAR10890, AAR10909, AAR10910 and AAQ10783.
CC
XX
SQ Sequence 924 AA;

Query Match 75.4%; Score 43; DB 12; Length 924;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKLEAE 12
   || |||||:|
Db 422 FLNlnkelgae 433

RESULT 5
AAR42385
ID AAR42385 standard; Protein: 924 AA.
XX
AC AAR42385;
XX
DT 19-APR-1994 (first entry)
XX
DE Recombinant leukotoxin peptide from plasmid PCR28.
XX
KM Haemophilus somnus; immunogenic; haemolysin; lppB; lppC;
KM thromboembolic meningoencephalitis; septicemia; arthritis;
KM pneumonia; lktA gene; haemin-binding protein; fusion protein.
XX
OS Pasteurella haemolytica.
XX
PN WO9321323-A.

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XX
PD 28-OCT-1993.
XX
PF 05-APR-1993; 93WO-CA00135.
XX
PR 09-APR-1992; 92US-0865050.
PR 04-JUN-1992; 92US-0893424.
PR 04-JUN-1992; 92US-0893426.
PR 29-MAR-1993; 93US-0038287.
PR 29-MAR-1993; 93US-0038288.
XX
PA (UYSA-) UNIV SASKATCHEWAN.
XX
PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
PI Rioux C, Theisen M;
XX
DR WPI; 1993-351733/44.
DR N-PSDB; AAQ51086.
XX
PT Haemophilus somnus immunogenic proteins used in vaccines -
PT selected from haemin-binding protein, haemolysin, lppB and lppC,
PT and corresp. DNA
XX
PS Disclosure; Fig 11; 119pp; English.
XX
CC The lppB gene protein was expressed in E. coli as a fusion to the
CC Pasteurella haemolytica leukotoxin gene lktA coded for by plasmid
CC pAA352. The lppB gene fragment was taken from pMS11. lppB can be
CC used in vaccines for preventing or treating H. somnus infections,
CC which cause thromboembolic meningo-encephalitis, septicemia, arthritis
CC and pneumonia in vertebrates.
CC See also AAR42370-86.
XX
SQ Sequence 924 AA;

Query Match 75.4%; Score 43; DB 14; Length 924;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKLEAE 12
   || |||||:|
Db 424 FLNlnkelgae 435

RESULT 6
AAR42380
ID AAR42380 standard; Protein: 924 AA.
XX
AC AAR42380;
XX
DT 19-APR-1994 (first entry)
XX
DE Recombinant leukotoxin peptide (split) from plasmid pGCH4.
XX
KM Haemophilus somnus; immunogenic; haemolysin; lppB; lppC;
KM thromboembolic meningoencephalitis; septicemia; arthritis;
KM pneumonia; lktA gene; haemin-binding protein; fusion protein.
XX
OS Pasteurella haemolytica.
XX
PN WO9321323-A.
XX
PD 28-OCT-1993.
XX
PF 05-APR-1993; 93WO-CA00135.
PR 09-APR-1992; 92US-0865050.
PR 04-JUN-1992; 92US-0893424.
PR 04-JUN-1992; 92US-0893426.
PR 29-MAR-1993; 93US-0038287.
PR 29-MAR-1993; 93US-0038288.

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PR 29-MAR-1993; 93US-0038719.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
 PI Rioux C, Theisen M;
 XX
 DR WPI; 1993-351733/44.
 DR N-PSDB; AAQ51082.
 XX
 PT Haemophilus somnus immunogenic proteins used in vaccines -
 PT selected from haemin-binding protein, haemolysin, LppB and LppC,
 PT and corresp. DNA
 XX
 PS Disclosure; Fig 6; 119pp; English.
 CC The hmb gene encoding the haemin-binding protein was expressed in
 CC E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene
 CC Ikta coded for by plasmid pAA352. The hmb gene fragment was taken
 CC from PRAP504 and starts at the codon for the 33 rd amino acid residue
 CC of ORF1. The haemin binding protein can be used in vaccines for
 CC preventing or treating H. somnus infections, which cause thromboembolic
 CC meningo-encephalitis, septicemia, arthritis and pneumonia in
 CC vertebrates.
 CC See also AAR42370-86.
 XX
 SQ Sequence 924 AA;
 Query Match 75.4%; Score 43; DB 14; Length 924;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FLSLNKKEAE 12
 || |||||:
 Db 424 fllnlknlqae 435

RESULT 7
 AAR42378
 ID AAR42378 standard; Protein; 924 AA.
 XX
 AC AAR42378;
 XX
 DT 19-APR-1994 (first entry)
 XX
 DE Recombinant leukotoxin peptide (SPLT) from plasmid pGCH5.
 XX
 KW Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;
 KW thromboembolic meningoencephalitis; septicemia; arthritis;
 KW pneumonia; Ikta gene; haemin-binding protein; fusion protein.
 XX
 OS Pasteurella haemolytica.
 XX
 PN W09321323-A.
 XX
 PD 28-OCT-1993.
 XX
 PF 05-APR-1993; 93WO-CA00135.
 XX
 PR 09-APR-1992; 92US-0865050.
 PR 04-JUN-1992; 92US-0893424.
 PR 04-JUN-1992; 92US-0893426.
 PR 29-MAR-1993; 93US-0038287.
 PR 29-MAR-1993; 93US-0038288.
 PR 29-MAR-1993; 93US-0038719.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
 PI Rioux C, Theisen M;
 XX
 DR WPI; 1993-351733/44.

DR N-PSDB; AAQ51081.
 XX
 PT Haemophilus somnus immunogenic proteins used in vaccines -
 PT selected from haemin-binding protein, haemolysin, LppB and LppC,
 PT and corresp. DNA
 XX
 PS Disclosure; Fig 5; 119pp; English.
 CC The hmb gene encoding the haemin-binding protein was expressed in
 CC E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene
 CC Ikta coded for by plasmid pAA352. The hmb gene fragment was taken
 CC from PRAP501 and starts at the codon for the third amino acid residue
 CC of ORF1. The haemin binding protein can be used in vaccines for
 CC preventing or treating H. somnus infections, which cause thromboembolic
 CC meningo-encephalitis, septicemia, arthritis and pneumonia in
 CC vertebrates.
 CC See also AAR42370-86.
 XX
 SQ Sequence 924 AA;
 Query Match 75.4%; Score 43; DB 14; Length 924;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FLSLNKKEAE 12
 || |||||:
 Db 424 fllnlknlqae 435

RESULT 8
 AAR14482
 ID AAR14482 standard; Protein; 926 AA.
 XX
 AC AAR14482;
 XX
 DT 15-JAN-1992 (first entry)
 XX
 DE LKT352.
 XX
 KW Antigen; leukotoxin; vaccine; Ikta.
 XX
 OS Pasteurella haemolytica.
 XX
 PN W09115237-A.
 XX
 PD 17-OCT-1991.
 XX
 PF 17-OCT-1991; 91WO-CA00170.
 XX
 PR 05-APR-1990; 90US-0504850.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Acres SD, Bariuk LA, Potter AA, Lawman MJP;
 XX
 DR WPI; 1991-324967/44.
 XX
 PT Vaccines for Pasteurella haemolytica infection in cattle -
 PT comprise sub-unit antigens from P haemolytica fimbrial protein,
 PT plasmid receptor, 50 K outer membrane protein and leukotoxin.
 XX
 PS Disclosure; Fig 5; 92pp; English.
 CC LKT352 is 98% homologous with authentic leukotoxin and migrates
 CC to the same position on gels.
 CC The LKT352 gene was prep'd. as follows: Ikta, an MaeI fragment
 CC contg. the gene was ligated into the SmaI site of pUC13 to form
 CC pAA179. From this, two constructs were made in the pTac-based
 CC vector, pGH432:lact digested with SmaI. One, pAA342, consisted of
 CC the 5' Ahairi fragment from Ikta while the other, pAA345, contained
 CC the entire MaeI fragment. Clone pAA342 expressed a truncated
 CC leukotoxin peptide at high levels while pAA345 expressed full

CC length leukotoxin at very low levels. The 3' end of the lktA gene
 CC of pAA345 was therefore ligated to StyI/BamHI digested pAA342 to
 CC yield pAA352 contg. the lkt352 sequence. The protein expressed
 CC from the vector can be used to prepare a subunit vaccine with
 CC other P. haemolytica antigens, e.g. fibrinolytic protein, plasmin
 CC receptor or 50K outer membrane protein. The vaccines can be used
 CC to protect cattle from respiratory diseases such as pneumonia, esp.
 CC shipping fever pneumonia.
 CC See also AAR14481, 83,84 and 85.
 XX
 SQ Sequence 926 AA:

Query Match 75.4%; Score 43; DB 12; Length 926;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
 || |||||:
 Db 424 flInlnkelgae 435

RESULT 9

AAR34545
 ID AAR34545 standard; Protein: 926 AA.

XX
 AC AAR34545:

XX 23-AUG-1993 (first entry)

XX Leukotoxin 352 produced from pAA352.

DE Vector: LKT 352; flanking; recombinant; antigen; somatostatin;

KM gonadotropin releasing hormone; rotavirus viral protein 4;

XX carrier protein; laccation; reproduction.

OS Pasteurella haemolytica.

XX WO9308290-A.

XX 29-APR-1993.

XX 15-OCT-1992; 92WO-CA00449.

XX 16-OCT-1991; 91US-0779171.

XX 14-OCT-1992; 92US-0960932.

XX (UYSA-) UNIV SASKATCHEWAN.

XX Hughes HPA, Potter AA, Redmond MJ;

XX WPI; 1993-152482/18.

XX N-PSDB; AAQ41317.

XX Immunological carrier system with enhanced immunogenicity -

XX comprises chimeric protein comprising leuco:toxin peptide or

XX homologous protein fused to antigen esp. somatostatin or

XX gonadotropin releasing hormone

XX Disclosure; Fig 3; 95pp; English.

XX Gene libraries of P. haemolytica A1 (strain B122) were constructed

XX in lambda gIII and pUC13. Resulting clones were used to transform E.

XX coli and individual colonies were pooled and screened for reaction

XX with serum from a calf which had survived a P. haemolytica infection

XX and that had been boosted with a conc. culture supernatant of P.

XX haemolytica to increase anti-leukotoxin antibody levels. Positive

XX colonies were screened for their ability to produce leukotoxin by

XX incubating cell lysates with bovine neutrophils and measuring the

XX release of lactate dehydrogenase from the neutrophils. A 4kb

XX fragment was obd. Progressively larger clones were isolated by

XX chromosome walking to isolate full length recombinants of ca. 8kb.

XX In pAA114. The clone was subjected to restriction enzyme digestion

CC to yield two clones, one expressing truncated leukotoxin peptide at
 CC high levels and the other expressing the full length leukotoxin at
 CC low levels. The 3' end of the lktA gene from the full length clone
 CC was ligated to the truncated gene clone to yield plasmid pAA352. The
 CC clone was used to produce chimeric proteins by gene fusion with an
 CC antigen coding sequence, e.g. the coding sequence of somatostatin,
 CC gonadotropin releasing hormone or rotavirus viral protein 4, i.e.
 CC leukotoxin works as a carrier protein to bring about a larger
 CC immune response than the antigen alone. Immunisation with these
 CC antigens can regulate growth rate, laccation and reproductive
 CC efficiency. See also AAR34546-8.
 XX
 SQ Sequence 926 AA:

Query Match 75.4%; Score 43; DB 14; Length 926;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
 || |||||:
 Db 424 flInlnkelgae 435

RESULT 10

AAR50291
 ID AAR50291 standard; Protein: 926 AA.

XX
 AC AAR50291:

XX 06-OCT-1994 (first entry)

XX Recombinant leukotoxin from plasmid pAA352.

DE Vaccine; outer membrane protein; OMP; Haemophilus somnus;

KM iron regulated protein; leukotoxin; Pasteurella haemolytica;

XX LKT352.

XX Pasteurella haemolytica A1 (strain B122).

XX CA2099707-A.

XX 03-JAN-1994.

XX 29-JUN-1993; 93CA-2099707.

XX 02-JUL-1992; 92US-0908253.

XX (UYSA-) UNIV SASKATCHEWAN.

XX Harland RJ, Potter AA;

XX WPI; 1994-092909/12.

XX N-PSDB; AAQ44760.

XX Haemophilus somnus outer membrane protein extract -

XX enriched with iron-regulated proteins, opt. contg.

XX leuco:toxin antigens, for use as vaccine

XX Claim 5; Fig 5; 78pp; English.

XX A vaccine comprising an outer membrane protein (OMP) extract of

XX Haemophilus somnus enriched with iron regulated proteins is new.

XX The vaccine pref. further comprises an immunogenic leukotoxin

XX polypeptide, esp. an immunogenic Pasteurella haemolytica leukotoxin

XX homologous to LKT352. Example 1.2 describes the prodn. of

XX P. haemolytica recombinant leukotoxin from pAA352.

XX Two expression constructs were made. One, pAA342, contained the

XX 5'-AhaII fragment of the lktA gene, while the other, pAA345,

XX contained the entire lktA gene. pAA342 expressed a truncated

XX leukotoxin peptide at high levels, while pAA345 expressed full

XX length leukotoxin at very low levels. Therefore, the 3' end

XX of the lktA gene was ligated into pAA342, yielding plasmid pAA352.

CC LKT352 or new leukotoxin is 98% homologous to authentic
 CC leukotoxin.
 CC NB: the protein sequence in Fig 5 comprises 926 amino acids,
 CC however this protein is described in the text as having
 CC 931 amino acids.
 XX
 SQ Sequence 926 AA;

Query Match 75.4%; Score 43; DB 15; Length 926;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
 DB 424 fllnlknlqae 435

RESULT 11

AAW03945
 ID AAW03945 standard; Protein; 926 AA.

AC AAW03945;

DT 20-NOV-1996 (first entry)

DE P. haemolytica truncated leukotoxin (LKT352).

KW Leukotoxin; LKT; gonadotropin-releasing hormone; GnRH;
 fusion protein; immunogen; vaccine; fertility control;
 KW contraceptive; sterilisation; plasmid pAA352.

OS Pasteurella haemolytica AI strain B122.

PN W09624675-A1.

PD 15-AUG-1996.

PF 24-JAN-1996; 96WO-CA00049.

PR 10-FEB-1995; 95US-0387156.

PA (UYSA-) UNIV SASKATCHEWAN.

PI Manns JG, Potter AA;

DR WPI; 1996-384447/38.

DR N-PSDB; AAT37179.

PT Gonadotropin-releasing hormone multimer fusion proteins - with
 leukotoxin polypeptide for increased immunogenicity, useful in
 antileukemia vaccine prodn.

PS Example 1; Fig 3A-3i; 87pp; English.

CC A truncated leukotoxin (AAW03945). LKT 352, lacks the cytotoxic
 CC portion of the native protein from Pasteurella haemolytica. It is
 CC the product of plasmid pAA352 which carries a truncated lktA gene
 CC (AAT37179). A fusion protein (AAW03942) between LKT352 and a
 CC gonadotropin releasing hormone tetramer can be expressed in
 CC Escherichia coli. This is useful as a vaccine for fertility
 CC control, parit. Immunological sterilisation of domestic or
 CC farm animals.

SQ Sequence 926 AA;

Query Match 75.4%; Score 43; DB 17; Length 926;
 Best Local Similarity 75.0%; Pred. No. 52;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
 DB 424 fllnlknlqae 435

DB 424 fllnlknlqae 435

RESULT 12

AAW79568
 ID AAW79568 standard; Protein; 926 AA.

AC AAW79568;

DT 24-DEC-1998 (first entry)

DE Leukotoxin 352 polypeptide.

KW Gonadotropin releasing hormone; GnRH; chimera; leukotoxin polypeptide;
 multimer; vaccine; tumour; Leukotoxin 352; LKT 352; lktA; plasmid pAA352;
 KW cytotoxic.

OS Synthetic.

FT Key Location/Qualifiers

FT Misc_feature 11.924
 /note="Recombinant leukotoxin peptide"

PN W09806848-A1.

PD 19-FEB-1998.

PF 08-AUG-1997; 97WO-CA00559.

PR 09-AUG-1996; 96US-0694865.

PA (UYSA-) UNIV SASKATCHEWAN.

PI Manns JG, Potter AA;

DR WPI; 1998-159540/14.

DR N-PSDB; AAV61530.

PT Chimeric protein of leukotoxin and gonadotropin releasing hormone -
 useful for, e.g. preparation of vaccines for reduction of incidence
 of mammary tumours in mammals

PS Claim 7; Figure 3.1-9; 118pp; English.

CC The present sequence represents a recombinantly produced or chemically
 CC synthesised leukotoxin 352 (LKT 352) polypeptide, derived from the lktA
 CC gene that is present in the plasmid pAA352. This gene produces a
 CC truncated protein that has an estimated molecular weight of about 99 kDa
 CC and lacks the cytotoxic portion of the molecule. Thus this gene has a
 CC higher expression level than that of the full-length molecule. This can
 CC be used in the construction of a chimeric protein that comprises a
 CC leukotoxin polypeptide, several multimers, and a GnRH sequence. The
 CC chimeric protein can be used as a vaccine to help reduce the incidence of
 CC mammary tumours in a mammalian individual.

SQ Sequence 926 AA;

Query Match 75.4%; Score 43; DB 19; Length 926;
 Best Local Similarity 75.0%; Pred. No. 52;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
 DB 424 fllnlknlqae 435

RESULT 13

AAAR34547
 ID AAR34547 standard; Protein; 936 AA.

XX AAR34547;
 XX

DT 23-AUG-1993 (first entry)
 XX
 DE GNRH-leukotoxin gene fusion prod.
 XX
 KW Vector; LKT 352; flanking; recombinant; antigen; somatostatin;
 KW gonadotropin releasing hormone; rotavirus viral protein 4;
 KW carrier protein; lactation; reproduction; SRIF.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..926
 FT /note="recombinant leukotoxin protein"
 FT Peptide 927..936
 FT /note="GNRH"
 XX
 FT MO9308290-A.
 XX
 PN 29-APR-1993.
 PD
 XX
 PF 15-OCT-1992; 92WO-CA00449.
 XX
 PR 16-OCT-1991; 91US-0779171.
 PR 14-OCT-1992; 92US-0960932.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Hughes HPA, Potter AA, Redmond MJ;
 PI
 DR WPI; 1993-152482/18.
 DR N-PSDB; AAQ41322.
 XX
 PT Immunological carrier system with enhanced immunogenicity -
 PT comprises chimeric protein comprising leuco:toxin peptide or
 PT homologous protein fused to antigen esp. somatostatin or
 PT gonadotropin releasing hormone
 XX
 PS Example 2; Fig 8; 95pp; English.
 XX
 CC Oligonucleotides contg. sequences from bovine gonadotropin
 CC releasing hormone (GNRH) gene were constructed on a Pharmacia Gene
 CC Assembler using standard phosphoramidite chemistry. The oligo-
 CC nucleotides were annealed and ligated into vector PAA352 (contg.
 CC the Pateurella haemolytica leuko-toxin gene) which had been digested
 CC with BamHI. The ligated DNA was used to transform E. coli strain
 CC MH3000. Transformants contg. the oligonucleotide inserts were
 CC identified by restriction endonuclease mapping and the recombinant
 CC plasmid designated PAA502. The chimeric protein produced from the
 CC plasmid works to bring about a larger immune response than the antigen
 CC alone, i.e. the leukotoxin works as a carrier protein.
 CC See also AAR34545-8.
 CC
 XX
 SQ Sequence 936 AA;
 XX

Query Match 75.4%; Score 43; DB 14; Length 936;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 FLSLNKLEAE 12
 Db 424 flnlhkelgae 435

RESULT 14
 AAR34546
 ID AAR34546 standard; Protein; 943 AA.
 XX
 AC AAR34546;
 XX
 DT 23-AUG-1993 (first entry)
 XX
 DE Somatostatin-leukotoxin gene fusion prod.

XX
 KW Vector; LKT 352; flanking; recombinant; antigen; somatostatin;
 KW gonadotropin releasing hormone; rotavirus viral protein 4;
 KW carrier protein; lactation; reproduction; SRIF.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..929
 FT /note="recombinant leukotoxin protein"
 FT Peptide 930..943
 FT /note="SRIF"
 XX
 FT MO9308290-A.
 XX
 PN 29-APR-1993.
 PD
 XX
 PF 15-OCT-1992; 92WO-CA00449.
 XX
 PR 16-OCT-1991; 91US-0779171.
 PR 14-OCT-1992; 92US-0960932.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Hughes HPA, Potter AA, Redmond MJ;
 PI
 DR WPI; 1993-152482/18.
 DR N-PSDB; AAQ41321.
 XX
 PT Immunological carrier system with enhanced immunogenicity -
 PT comprises chimeric protein comprising leuco:toxin peptide or
 PT homologous protein fused to antigen esp. somatostatin or
 PT gonadotropin releasing hormone
 XX
 PS Example 2; Fig 6; 95pp; English.
 XX
 CC Oligonucleotides contg. sequences from bovine somatostatin (SRIF)
 CC gene were constructed on a Pharmacia Gene Assembler using standard
 CC phosphoramidite chemistry. The oligonucleotides were annealed and
 CC ligated into vector PAA352 (contg. the Pateurella haemolytica leuko-
 CC toxin gene) which had been digested with BamHI. The ligated DNA was
 CC used to transform E. coli strain JM105. Transformants contg. the
 CC oligonucleotide inserts were identified by restriction endonuclease
 CC mapping and the recombinant plasmid designated PAA496. The
 CC chimeric protein produced from the plasmid works to bring about a
 CC larger immune response than the antigen alone, i.e. the leukotoxin
 CC works as a carrier protein.
 CC See also AAR34545-8.
 CC
 XX
 SQ Sequence 943 AA;
 XX

Query Match 75.4%; Score 43; DB 14; Length 943;
 Best Local Similarity 75.0%; Pred. No. 53;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 FLSLNKLEAE 12
 Db 424 flnlhkelgae 435

RESULT 15
 AAR34548
 ID AAR34548 standard; Protein; 951 AA.
 XX
 AC AAR34548;
 XX
 DT 23-AUG-1993 (first entry)
 XX
 DE Rotavirus VP4-leukotoxin gene fusion prod.
 XX
 KW Vector; LKT 352; flanking; recombinant; antigen; somatostatin;
 KW gonadotropin releasing hormone; rotavirus viral protein 4;

XX	Carrier protein; lactation; reproduction; SRIF	
OS	Synthetic.	
XX		
XX	Key	Location/Qualifiers
XX	Protein	1..926
XX		/note= "recombinant leukotoxin protein"
XX	Peptide	927..951
XX		/note= "Rotavirus VP-4"
XX		
XX	W09308290-A.	
XX		
XX	29-APR-1993.	
XX		
XX	15-OCT-1992;	92WO-CA00449.
XX		
XX	16-OCT-1991;	91US-0779171.
XX	14-OCT-1992;	92US-0960932.
XX		
XX	(UYSA-) UNIV SASKATCHEWAN.	
XX		
XX	Hughes HPA, Potter AA, Redmond MJ;	
XX		
XX	WPI: 1993-152482/18.	
XX	N-PSDB: AAQ41322.	
XX		
XX	Immunological carrier system with enhanced immunogenicity -	
XX	comprises chimeric protein comprising leucotoxin peptide or	
XX	homologous protein fused to antigen esp. somatostatin or	
XX	gonadotropin releasing hormone	
XX		
XX	Example 2: Fig 8; 95pp; English.	
XX		
XX	Oligonucleotide conty. sequences from bovine Rotavirus Viral	
XX	protein 4 (VP-4) gene were constructed on a Pharmacia Gene	
XX	Assembler using standard phosphoramidite chemistry. The oligo-	
XX	nucleotides were annealed and ligated into vector pAA52 (conty.	
XX	the Pateurella haemolytica leuko-toxin gene) which had been digested	
XX	with BamHI. The ligated DNA was used to transform E. coli strain	
XX	MH3000. Transformants conty. the oligonucleotide inserts were	
XX	identified by restriction endonuclease mapping and the recombinant	
XX	plasmid designated pAA501. The chimeric protein produced from the	
XX	plasmid works to bring about a larger immune response than the antigen	
XX	alone, i.e. the leukotoxin works as a carrier protein.	
XX	See also AAR34545-7.	
XX		
XX	Sequence 951 AA;	

Query Match	75.4%	Score 43	DB 14	Length 951
Best Local Similarity	75.0%	Pred. No. 53		
Matches	9	Conservative	1	Mismatches 2
				Indels 0
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QY	1	FLSELNKELEAE	12	
Db	424	flinkelgae	435	

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6	1928	41.5	1049	1	S51784
7	1851.5	39.9	1024	2	S10056
8	1849	39.8	1023	1	LEECA
9	1820	39.2	1055	1	A37305
10	1767.5	38.0	1022	1	I39643
11	1752	37.7	998	2	T00227
12	1733	37.4	998	2	I41078
13	809.5	17.3	1705	2	S16167
14	806	17.3	1706	1	OYBRC
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18	411	8.8	1302	2	C82779
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21	391	8.4	2064	2	G82562
22	383	8.2	208	2	S34238
23	365	7.9	697	2	F81856
24	343	7.4	4936	2	AH2515
25	332.5	7.2	1944	2	AH3098
26	332.5	7.2	1990	2	A96188
27	338.5	7.1	1296	2	C82521
28	305.5	6.6	993	2	AE1905
29	304.5	6.6	1072	2	G95831

30	287.5	6.2	308.3	2	AG2493	hypothetical prote
31	287	6.2	1417	2	AG2137	hypothetical prote
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33	280	6.0	900	2	AC1852	hypothetical prote
34	276	5.9	650	2	CG7572	calcium-binding pr
35	266.5	5.8	1112	2	H95964	probable outer mem
36	268	5.8	359	2	CG9405	hypothetical prote
37	267.5	5.8	387	2	E95995	hypothetical calci
38	266.5	5.7	589	2	AD2263	hypothetical prote
39	266	5.7	2348	2	AD1841	hypothetical prote
40	263.5	5.7	387	2	E95933	probable calcium-b
41	262.5	5.7	1741	2	SW4910	hemolysin - synech
42	262.5	5.7	3262	2	AH2137	hypothetical prote
43	261.5	5.6	1839	2	SW7626	mannuronan C-5-epi
44	260	5.6	1038	2	T03516	probable outer mem
45	259.5	5.6	219	2	B95953	probable secreted

ALIGNMENTS

```

RESULT      1
B30169
leukotoxin A - Pasteurella haemolytica (serotype 1)
N:Alternate names: lktA protein
C:Species: Pasteurella haemolytica
C:Date: 12-Oct-1999 #sequenceRevision 15-Nov-1996 #text_change 18-Jun-1999
C:Accession: B30169; C32051; S29516
R:Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.
DNA 8, 15-28, 1989
A:title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.
A:Reference number: A30169; MUID:89210283
A:Accession: B30169
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-953 <HIG>
R:Strathdee, C.A.; Lo, R.Y.C.
J. Bacteriol. 171, 916-928, 1989
A:title: Cloning, nucleotide sequence, and characterization of genes encoding the se
A:Reference number: A32051; MUID:89123172
A:Accession: C32051
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A:Molecule type: DNA
A:Residues: 947-953 <STR>
R:Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E.
Infect. Immun. 55, 1987-1996, 1987
A:title: Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica AI.
A:Reference number: S29515; MUID:87306837
A:Accession: S29516
A:Molecule type: DNA
A:Residues: 1-741, 'D', 743-953 <LOR>
A:Cross-references: EMBL:M20730; NID:g150492; PIDN:AAA25529.1; PID:g150494
C:Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
C:Genetics:
A:Gene: lktA
C:Function:
A:Description: lysates leukocytes
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytotoxic; exotoxin; hemolysis; lipoprotein; tandem rep
F:238-784/domain: hemolysin A homology <HXHA>
F:716-807/region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVITF]-X)
F:534/binding site: palmitate (lys) (covalent) status predicted

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Best Local Similarity 49.9%; Pred. No.1.6e-111;
Matches 464; Conservative 175; Mismatches 264; Indels 26; Gaps 13;

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Db      87 AQTSLGTOTAIIGTERGIVISAPQIDKLQK---TKAQALGSGAESIVONANKAKTVLS 143
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QY      186 LGSTISQAKGFSNIGNKLONL-NFSKTNLGEIITGLLSISAGFALADKNASTGKVA 244
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QY      245 GPELSNOYIGVNTKATISSVLAQRYAAGLSTTGANAALITSSIMLAISPLAFMAADKFN 304
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QY      305 HANALDEFKOFKRGYGDHLLAEYQGVGTIEASTITSTALCAVSAGVSAVAAYAV 364
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QY      365 GAPIALLVAGYTGILSIGILEASKAMFESVANRLOGKLTLEMEKONGGQNYEDKGYD 424
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QY      425 AVIANNKELSELNKELEAEVIAATQORNNNGELAGITKGRITSGKAYADAPEDG 484
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QY      485 KKEVAGSNITLDAKTGIDISNSNGKTOALHTFSPILTACSESRELTNGKYSYINKL 544
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QY      545 FGRYKNOVOTGEASSKIDESKVIORV-----AETEGTEGLIVAKAGNDIEVQ 597
Db      563 INRVDSMKITLGAASSTFDTLNVVQRIEELDNAGNVTKETKTIKILGEGDDNVFVS 622
QY      598 GKMNIDGGDGDHRYFYSDGFGNTTVGTSATEAGSTTVARKKARGLIYHEVYKQETK 657
Db      623 GTTELDDGEGDYRVHYSR-GNIGALTIDATKETEGETSVNFEVTGKALHEVSTHTAL 681
QY      658 VGRKTEITQYDYLKRYGYQSTDNLSYEEVIGSOFNVFKSKNDIFHSGEGDL 717
Db      682 VGNNEKELEYR-HSNQNHAGYTYTKDLKAVEIITGSHNDIFKSKNDAPNGSDYDT 740
QY      718 LDGAGADDRLFGKGNDRILSGDEGDDLLDGGSGDDVILNGAGANDYIFRKGDDNDLYD 777
Db      741 IYGNNGNDRILFGKGGDDLLDGGNGDDFDGCGKNDILHGGKGDIDFVHRKGGNDIIDS 800
QY      778 TGNKLAFAADNIDIMIERKEGELIVKRNHSGSINPRY---ITSNLQNYOSKNTD 833
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QY      894 LVGSMALFETGANSVSSNALQPIOTPOGI 922
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RESULT 2
 B33389
 toxin II - Actinobacillus pleuropneumoniae
 N:Alternate names: cytotoxin II; RTX-toxin II (AprXII)
 C:Species: Actinobacillus pleuropneumoniae
 C:Date: 09-Mar-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
 C:Accession: B33389; S18853; B43599
 R:Chang, Y.F.; Young, R.; Struck, D.K.
 DNA 8, 635-647, 1989
 A:Title: Cloning and characterization of a hemolysin gene from Actinobacillus (Haemophilus) pleuropneumoniae serotype 9.
 A:Reference number: A33389; MIMD:50126233
 A:Accession: B33389
 A:Molecule type: DNA

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A:Residues: 1-956 <CHA>
A:Cross-references: GB:M30602; NID:g141823; PIDN:AAA87232.1; PID:g141825
A:Experimental source: serotype 5
R:Smith, M.A.; Briatore, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, A.L.J.
submitted to the EMBL Data Library, July 1991
A:Description: Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
A:Reference number: S18852
A:Accession: S18853
A:Molecule type: DNA
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A:Cross-references: EMBL:X61111; NID:g38939; PIDN:CAA43423.1; PID:g38941
R:Smith, M.A.; Briatore, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, A.L.J.
Infect. Immun. 59, 4497-4504, 1991
A:Title: Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
A:Reference number: A43599; MIMD:92040145
A:Accession: B43599
A:Status: preliminary
A:Molecule type: DNA
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C:Comment: This organism causes porcine pleuropneumonia.
C:Genetics:
A:Gene: aprXII; appA; clytII
C:Function:
A:Description: attacks blood cell membranes and causes cell lysis
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytolysin; exotoxin; hemolysis; lipoprotein; tandem repeat; 243-787/Domain: hemolysin A homology <HYA>
F:243-787/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYIF]-X)
F:557/Binding site: palmitate (lys) (covalent) #status predicted

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Query Match 48.2%; Score 2240.5; DB 1; Length 956;
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Db      61 QGNGVQDLVKAAANDGIEVWREERSNDIARTSFPTTKILGFTDRGIVLPAQOLDNLK 120
QY      97 KHSYTRKLAGDSYVNDIRKLGKASNVLTSLSPFLGTALAGTEIDSLRKGDAPDALAK 156
Db      121 KNP--KIGNTIGSASISQIGNKANTVLGIGISLVSGLVSGVNLNELLQNDPNQLEAK 178
QY      157 ASIDLINEIIGNLSQSTOTIEAFSSQIAKLGSTTSQAKGFSNIGNKLONL-NFSKTNLGL 215
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QY      276 TGAVALAITSSIMLAISPLAFMAADKFNHANALDEFKOFKRGYGDHLLAEYQGVG 335
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Db      359 TIDASVTTINTFLAAISGCVGAASGSLVGAPVALLVAGVTGLITTYLEYSKQAMFEHVA 418
QY      396 NRLQGLIEMEKONGQVYFPDKGDSRYAAVLANLKLSELNKELEERYATITQQRWD 455
Db      419 NKVHRIYEWERKH-NKNYFEGYDSDRLADLODNMKELINLNKELOAEVIAITQQRWD 477
QY      456 NNIGELIATLGERIKSGRAYADAFEDGKRYVEGSGNTTLAKGIGITIDISNSNGKTOAL 515
Db      478 NOIGDLAISRTDKTISGKAYVDAFEQGHQSDSSVQDLNKKIINISNTN-RKTQSV 536
QY      516 HTSPILTACTESRELTNGKRYSYINKLFGKRVKNMUYTDEASSKIDFSKVIORVA--- 572

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Db 537 LEFTPLLTPEEENRERIOEGKNSYITKLHIORVDSWTVTDGDASSSDVDFNNVQRIAVKF 596
QY 573 -----EFGTDEIGLIYNAGAKNDIDFYGCKMNIIDGGDHDREYFKSDGFGNITVD 625
Db 597 DDAGNIEESDKV---IINLNGAGNDNVFSGSSTTVIDGGDGHDRHYSR-GEYGLAVID 652
QY 626 GTATAGSYTYVNRKVARGDYIEHVVKROETKGRKRTETIOYRDYELRKGYGYOSTDNL 685
Db 653 ATAFETKGSYVKRYVGDSCALHETATHTNOTNGNREKEIYR-REDDRHHTGYTITDLSL 711
QY 686 KSYEEVIGQFNDVFKSGKENDIFHSGEEDLLDGGAGDRLFGKGNDRLSGDEGDDL 745
Db 712 KSYEEIISQFNDIFKSGQEDVDFHGNVDTIDGNDGDHDLFGAGADVDVIDGNGCNFL 771
QY 746 DGGSGDDVLNGAGNDVYIFRKDGNIDLYDGTGNDKLAADANISDIIMEKREKGIYK 805
Db 772 VGGTGDIIISGKNDIYHKTGDBNDSTIDSGODKLAESDVLKDLFFKKYDSSLET- 830
QY 806 RNDHSSINIPRWY----ITSNLQNYOSNKTDRHIEOLIGKDGSIYTSQIDKTLQDKD 861
Db 831 INKGEKVRKGNMFLEDDLASTYANKAT-NDKKIEIITKGGERTISEQVDKLI--KEG 887
QY 862 GTVITSQELKKLADENKSOQLSASDIASSLNLKLVGSMALFGTANSVSN 910
Db 888 NNOISAEALSKVVDYNTSK-DRONVSNLSLAKLISSVGSFTSSDFRNN 935
RESULT 3
A35254
Leukotoxin A - Pasteurella haemolytica (serotype T10)
N:Alternate names: LkA protein
C:Species: Pasteurella haemolytica
C:Date: 10-Aug-1990 A:sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C:Accession: S37145; A35254; S34237; S34235
R:Lalison, A.F.; Alchison, K.; Donachie, W.
submitted to the EMBL Data Library, September 1993
A:Description: DNA sequence of the leukotoxin A gene from P. haemolytica T10 serotype.
A:Reference number: S37145
A:Accession: S37145
A:Molecule type: DNA
A:Residues: 1-955 <LA1>
A:Cross-references: EMBL:226247; NID:9400424; PIDN:CAA81206.1; PID:9400425
R:Highlander, S.K.; Engler, M.J.; Weinstein, G.M.
J. Bacteriol. 172, 2343-2350, 1990
A:Title: Secretion and expression of the Pasteurella haemolytica leukotoxin.
A:Reference number: A35254; M0ID:90236868.
A:Accession: A35254
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 950-955 <HTG>
A:Cross-references: GB:M24197; GB:M34943; GB:M34944
R:Lalison, A.F.; Alchison, K.D.; Donachie, W.
submitted to the EMBL Data Library, June 1993
A:Description: DNA sequence of the carboxy terminal end of leukotoxin A from the T3 sero
A:Reference number: S34235
A:Accession: S34237
A:Molecule type: DNA
A:Residues: 745-955 <LA2>
A:Cross-references: EMBL:222864; NID:9311828; PIDN:CAA80498.1; PID:9311829
A:Experimental source: serotype T3
A:Accession: S34235
A:Molecule type: DNA
A:Residues: 723-955 <LA3>
A:Cross-references: EMBL:222867; NID:9311824; PIDN:CAA80501.1; PID:9311825
A:Experimental source: serotype T10
C:Function:
A:Description: attacks cell membranes and causes cell lysis
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytotoxins; exotoxin; hemolysis; lipoprotein; tandem repeat;
F:240-786/Domain: hemolysin A homology <HLA>
F:718-809/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIVF]-X)
F:718-726/Region: repeat

F:727-735/Region: repeat
F:736-744/Region: repeat
F:745-753/Region: repeat
F:754-762/Region: repeat
F:763-771/Region: repeat
F:772-780/Region: repeat
F:781-789/Region: repeat
F:792-800/Region: repeat
F:801-809/Region: repeat
F:556/Binding site: palmitate (lys) (covalent) #status predicted
Query Match 48.1%; Score 2236; DB 1; Length 955;
Best local similarity 48.2%; Pred. No. 5,9e-107;
Matches 458; Conservative 178; Mismatches 271; Indels 44; Gaps 17;
QY 5 NTKSNIAQ---GLN-----STKGLKNLYATPKD--YDPOKGTLLNDFKAA 48
Db 12 NGIRSTLTATRGGINRAGSELTOAGOTLKNGAKKIILYIPKDYKSGSGNGLODLVKA 71
QY 49 DELGIARLAEPPHNETAKSVDPVNOFLSLTGTALISATKLEKFLQKSTNKLAGLD 108
Db 72 EELGIEYQKEEGNDIAKQTSLSGTIONVGLTERGIVLSAPQDLQK--NKVGALG 128
QY 109 SVENIDRKLGKASNVLTSSFLGTALAGIELDLSLIRKGDAAADALAKASIDLINEIGN 168
Db 129 SSESQTQNFQOAKTVLISGVGNSRTVLAGMDDEAL-QNESDQLTAKAGLELNSLIEN 187
QY 169 LSQSTQTEAFSSQLAKGSTISQANGFSNIGKNLQNL-NFSKTNLGLEITIGLSISA 227
Db 188 IANSVQTLDAFSEQISOFGSKLQNVKGLGALGKLNIGLDRAKGLDVKSRLLSGATA 247
QY 228 GFALADKNASTGKVVAGFELSNQVGNVKAISSVYLAORVAAAGSTGVAALLTSSI 287
Db 248 ALVLDADASTAKKVGFPFLAQVGNITKAAVSSYTLAORVAAAGSTGPVALLASTV 307
QY 288 MLAIISPLAFMAADKFNHANAALDEFKOPFRKFGYDGHDLAEYORGSTIEASTITISTA 347
Db 308 AVAISPLSFAGIADKPRASLSLEVYARFRKKGEGSLLAEVGHGCTIDASTALNTA 367
QY 348 LGAVSAGVSAAVGSAVAGDPIALLVAGVTGLISGLEPASKQAMFESYANRLQKILEMEK 407
Db 368 LAAIAGVSAAAGSVYASPIALLVSGITGVISITLQYKQAMEHVAANKIHNKIVEMEK 427
QY 408 QNGQNFEDKGYDSRYAAYLANNLKELSELKELAEARVATLQQRDNNTIGAGITKL 467
Db 428 NNGKNTFENGVDARYLANLDNNKFTLNLKELDAERVALITLQOQDWSNIGLAGISRL 487
QY 468 GERIKSGKAYADAFEDSKKVEAGSNITLDAKKTGIIDISNSNGKKTQALHFTSPLLTAGTE 527
Db 488 GEKVLSCAKAYDAFEEBQHLKAKQLVQDSAKGIIDVTNNGEAKTOHILFRPLLTGTE 547
QY 528 SRERLINGKSYINKLKFGRVKKMQVTDGEASSKLDFSKYIQVA-----ELEGDEI 580
Db 548 KREVRQYGYEYITKLHINVDWSQIKDGAASSFTDLTNVYORIGVELDAENVIKTKET 607
QY 581 GLIYNKAGNDIIFVGGCKNNIIOGSDGHDREYFSKDGSGFRTYDGSATPAGSYTNRK 640
Db 608 KIVATLGDGDNVFGVGTTEIDGEGEYDRVHNSR-GNYGALTDAKETEQGGSYTNRF 666
QY 641 VARGDIYHEVVKROETVGRKRTETIOYRDYELRKVGYGYOSTDLKSYEEVIGSQFNDV 700
Db 667 VESGKALHEGSTHTFTALVGNREKEIYR-HSNNOHNAAGYTKTKDLKAVEELIGSHNDIF 725
QY 701 KSGKFNDIFHSGEEDLLDGGAGDRLFGKGNDRLSGDEGDDLDDGSGDDVLNGAGN 760
Db 726 KSGKFNDAFNGCGVDITIDGNDGDRFLFGKGDDIIDGNGDDPIDGCKNDLLHGGKD 785
QY 761 DVIYIFKGGDNDLYDGTGNDKLAFAADANISDIIMEKREKGIYKRDHSGSINIPRWY- 819
Db 786 DIFVHRQDNDNSTIESEGDKLSFSDSNLKDILFFEKVGNHLYV-TTKQEKVYIQMFR 844
QY 820 ---ITSNLQNYOSNKTDRHIEOLIGKDGSIYTSQIDKLIQDKDGIVITSQELKLAD 876

[illegible]

Query Match 42.2%, Score 1959.5, DB 1, Length 1052;
Best Local Similarity 42.7%, Pred. No. 1e-92;
Matches 426: Conservative 166: Mismatches 286: Indels 119: Gaps 19:


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OY      8 KSNIOAGLNTKSGLK-----NLYLAIPKDYDPQKGLTNDFI 45
      19 KRAKKGYDTKNGLOYGVSQAKLQALAKAVOKGNKLVLPYKREYDSDVSGNGFPDVLV 78
OY      46 KAADELGIARLAEPNHTETAKKSVDTVNOFLSTGTGIAISATKLEKFLQKSTNKLAK 105
      79 KAADELGIQVKYVNRNLEVAHKSLSGTADQFLGTERGLTLFAPQLDQFLQKHSKISNV 138
OY      106 GLDSVENIDRKLGKASNVLTSLSPFGTALAGELDSLKLGKAAPDALAKASIDLINEI 165
      139 GSSTGVAVS-KLAKSQTIIISGIVSLGTVLGINLNAIISGSELE-LAEAGVSLASEL 196
OY      166 IGLSOSTOTIEAFSSOLAKTSTISOAKGFSNIGNKLQNLN--FSKTNLGEITITGL 222
      197 VSNIAAGTTTIDAFITQIQNGKLVENAKLGAGVGRQLOINSGALSKTGLDITISLL 256
OY      223 SGISAGFALADKNASTGKRYAAGFELSNOYIGNVTAKISSYVLAQRYAAGLSTTGAAVAL 282
      257 SGVTASFALANKNASTSTKVAAGFELSNOYIGGITKAVSSYTLAQRLAAGLSTTGPAAL 316
OY      283 ITSSIMLAISPLAFMNAADKFNANALDEPAKQPRKFGYGDHLLAEYORGVTIEASLT 342
      317 IASSISLAISPLAFLRVADNPNRSKEIGFAERFKLGYDGLKLSFEYHEAGTIDASIT 376
OY      343 TISTALGAVSAGVSAAGVAPIALVAGVTGLISGLEASKOAMFESVANRLQKI 402
      377 TISTALSALAGTAASAGALVGAAPITLVLTGTLISGLEFSKQMLDHVASKIGNKI 436
OY      403 LEMKONGCONYPDKGYDSRYAAYLANNLKFLSELNKELEAEVIAITQORNNIGELA 462
      437 DEMEKKY-GKNYFENGDAHKAFLBEDSFSLSPKNQYTERAVILITQORMEYIGELA 495
OY      463 GITKLEBRKSGAYADAPEDKKVEAG---SNITLDAKTGIIIDISNSKKTQALHFT 518
      496 GITKGDKSLSSGKAYVYDFEGKLEKPPDFSKVVPDPTKGEIDISNS--QSTLLKFEV 553
OY      519 SPLLTGTERERLTNGKYYSINKLFGKRVKMNQVDTG--EASSKLPFSKYIQR----- 570
      554 TPLLTGTERERLTNGKYYSINKLFGKRVKMNQVDTG--EASSKLPFSKYIQR----- 570
OY      571 VAETEGTDEIGLVYNAKAGNDIFVGGCKMNDGSDGHDHRYFSKDGCGFNITVDTGSAT 630
      613 VARGEERYREVRLVSHLGNKDVFLAAGSAEIIHAGEGHDVYVYDKT-DTGILVLDGTAKAT 671
OY      631 EAGSYVNRKVARG-DIYHEVYVRKQETKVKRKRTIQRDYELRKVG-YEYQSTDNLSKV 688
      672 EQRYSVTRELSGATKILREVINKNSAVGKRETELEYRDELTQSGNSMLKAHDELHAY 731
OY      689 EEYIGSOFNDVFGSKFNDIFHSGEGDLDLDGAGDRLFGGKGNDRLSGDEG----- 742
      732 EEIIGSNQDRDEFKSGFRDIFHAGADGDDLLNGNDGDDILVGDKNDELKRGDNGDQLYGG 791
OY      743 -----DILLDGSGGDV 753
      792 EGNDKLLGNGNMYLSGGDGNDELQVLGNGFNVLRGKGDDKLYGSSGSDLLDGGEGNDY 851
OY      754 LAGGAGNDVYIFPKGDGNDTLVY--GTGDKLAFADANISIMIERTEKGIIVKRNDS 810
      852 LLEGGDSDFYVYSTGSHNHTIYDGKSSDDKLYLSDFSFDRLLVEKVDNLVLRSESS 911
OY      811 ---GSIINIPRWYITSNQONQSKTDHKEQLGKOSYITTSQIDKIIDKKDGYIYS 867
      912 HNNGVLTIKWF-----KEGKNYVNRKTIQIYDKNGRKTIAENLGTGYFKNAPKADNLLN 964
OY      868 QELKTLADENKSOGLSASDIASLNLKLVGSMALFGTA 904
      965 YATKE--DQNES--NLSLKTLSKITITNAGNFGVA 996

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RESULT 6
S51784
toxin III - Actinobacillus pleuropneumoniae (serotype 2)

N:Alternate names: RTX-toxin IIIA (ApXIIIa)
C:Species: Actinobacillus pleuropneumoniae
C>Date: 14-Jul-1995 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C/Accession: S51784
R:Chang, Y.F.; Shi, J.; Ma, D.P.; Shin, S.J.; Lein, D.H.
DNA Cell Biol. 12, 351-362, 1993
A>Title: Molecular analysis of the Actinobacillus pleuropneumoniae RTX toxin-III gene
A/Reference number: S51783; MIDID:93263992
A/Accession: S51784
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1049 <CHA>
A/Cross-references: EMBL:L12145; NID:9349605; PIDN:AAA21924.1; PID:9470685
C/Comment: This organism causes porcine pleuropneumonia.
C/Genetics:
A/Gene: apXIIIa
C/Function:
A/Description: lyses lung macrophages
C/Superfamily: hemolysin A; hemolysin A homology
C/Keywords: calcium binding; cytotoxins; exotoxin; lipoprotein; tandem repeat; thioles
F:254-803/Domain: hemolysin A homology <HLVA>
F:735-861/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYIF]-X)
F:571,702/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 41.5%; Score 1928; DB 1; Length 1049;

Best Local Similarity 43.1%; Pred. No. 4.1e-91;

Matches 429; Conservative 152; Mismatches 295; Indels 120; Gaps 21;

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OY      8 KSNIOAGLNTKSGLK-----NLYLAIPKDYDPQKGLTNDFI 45
      19 KRAKKGYDTKNGLOYGVSQAKLQALAKAVOKGNKLVLPYKREYDSDVSGNGFPDVLV 78
OY      46 KAADELGIARLAEPNHTETAKKSVDTVNOFLSTGTGIAISATKLEKFLQKSTNKLAK 105
      79 KAADELGIQVKYVNRNLEVAHKSLSGTADQFLGTERGLTLFAPQLDQFLQKHSKISNV 138
OY      106 GLDSVENIDRKLGKASNVLTSLSPFGTALAGELDSLKLGKAAPDALAKASIDLINEI 165
      139 GSSTGDAVS-KLAKSQTIIISGIVSLGTVLGINLNAIISGSELE-LAEAGVSLASEL 196
OY      166 IGLSOSTOTIEAFSSOLAKTSTISOAKGFSNIGNKLQNLN--FSKTNLGEITITGL 222
      197 VSNIAAGTTTIDAFITQIQNGKLVENAKLGAGVGRQLOINSGALSKTGLDITISLL 256
OY      223 SGISAGFALADKNASTGKRYAAGFELSNOYIGNVTAKISSYVLAQRYAAGLSTTGAAVAL 282
      257 SGVTASFALANKNASTSTKVAAGFELSNOYIGGITKAVSSYTLAQRLAAGLSTTGPAAL 316
OY      283 ITSSIMLAISPLAFMNAADKFNANALDEPAKQPRKFGYGDHLLAEYORGVTIEASLT 342
      317 IASSISLAISPLAFLRVADNPNRSKEIGFAERFKLGYDGLKLSFEYHEAGTIDASIT 376
OY      343 TISTALGAVSAGVSAAGVAPIALVAGVTGLISGLEASKOAMFESVANRLQKI 402
      377 TISTALSALAGTAASAGALVGAAPITLVLTGTLISGLEFSKQMLDHVASKIGNKI 436
OY      403 LEMKONGCONYPDKGYDSRYAAYLANNLKFLSELNKELEAEVIAITQORNNIGELA 462
      437 DEMEKKY-GKNYFENGDAHKAFLBEDSFSLSPKNQYTERAVILITQORMEYIGELA 495
OY      463 GITKLEBRKSGAYADAPEDKKVEAG---SNITLDAKTGIIIDISNSKKTQALHFT 518
      496 GITKGDKSLSSGKAYVYDFEGKLEKPPDFSKVVPDPTKGEIDISNS--QSTLLKFEV 553
OY      519 SPLLTGTERERLTNGKYYSINKLFGKRVKMNQVDTG--EASSKLPFSKYIQR----- 570
      554 TPLLTGTERERLTNGKYYSINKLFGKRVKMNQVDTG--EASSKLPFSKYIQR----- 570
OY      571 VAETEGTDEIGLVYNAKAGNDIFVGGCKMNDGSDGHDHRYFSKDGCGFNITVDTGSAT 630
      613 VARGEERYREVRLVSHLGNKDVFLAAGSAEIIHAGEGHDVYVYDKT-DTGILVLDGTAKAT 671

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QY 631 EAGSYTVNRKVARG-DIYHEVVKROETKRTETIOYRDYELRKVG-IGYOSTDMLKSY 688
 Db 672 EGRYVTRRLSGATILREVIKNOXYAVGKRETELEYRDTLQSGNSMLKADHLHSV 731
 QY 689 EEVYISGFNDVFKSGFNDIFHSGEGDDLLDGGAGDDRLFGCGKGNRLSGD----- 739
 Db 732 EE-IGSNORDEFKSGFRDIFHGADGDDLLNGNDGDDILYCGKGNDELKGNNDLLYGG 790
 QY 740 EGD-----DLDDGSGGDDY 753
 Db 791 EGDGDKLLGNGNNYLSGGGDNDELQVLGNGFVNLRGKGGDDKLYGSSGSDLLDGGEGNDY 850
 QY 754 LNGAGANDYIFRKGGNDLYD---GTGNDKLAFADANISDMIRTEGIIIVK--RND 808
 Db 851 LGGGDSDFYVYRSTSGNTITIDOGASDSKLYLSDLSFDMLVKRVNDLEFRSNNNS 910
 QY 809 HGSINIPWYITSNLQNYOSKNTDHIKIDOLGKDSYITTSODIKLIDCKDGYITTSQ 868
 Db 911 NSGVILIKDMFKGGSYN-----HKIQIVDKNGRKLTACNLGNPHD-----TQOASS 959
 QY 869 ELKRLADENKSGKLSASDIASSLNKLYGSMALFGTA 904
 Db 960 LKNTQOEONESNLSS--LKTELKITTINAGNFVA 993

RESULT 7
 hemolysin A - Escherichia coli plasmid phly152
 C:Species: Escherichia coli
 C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 04-Mar-2000
 C:Accession: S10056
 R:Hess, J.; Wels, W.; Vogel, M.; Goebel, W.
 FEMS Microbiol. Lett. 34, 1-11, 1986
 A:Title: Nucleotide sequence of a plasmid-encoded hemolysin determinant and its comparison
 A:Reference number: S07209
 A:Accession: S10056
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1024 <HES>
 A:Cross-references: EMBL:M14107
 C:Genetics:
 A:Genome: plasmid phly152
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: lipoprotein
 F:247-792/Domain: hemolysin A homology <HLVA>
 F:364,690/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 39.9%; Score 1851.5; DB 2; Length 1024;
 Best Local Similarity 41.3%; Pred. No. 3,4e-87;
 Matches 426; Conservative 153; Mismatches 308; Indels 139; Gaps 24;

QY 7 IKSNIQAGL-----NSTKSGLK-----NLYLIPKDYDPQKGTINDF 44
 Db 9 IKSTLQSAKQSAANKLHSAAGSTKDALKAKEQTRNAGNRLITLIPDYKQ--GSSINDL 67
 QY 45 IKADELGIARLAEHPHHTTAKKSVDPVNOFLSLTQGLAISATKLEKFLQKH--GTNK 102
 Db 68 VRTADELGIEVOYDEKNGTATTKQVETAEKLGITFERGVITFAPQDKLLQKQKGN 127
 QY 103 LAKLDSVENIDRKLGASVNLSTLSEFLGATLALGILDSLTK---GMAAPDALAKAS 158
 Db 128 LGGG---AENIGDNLGKAGGILSTFQNFDTALSSMKIDELIKQKSGGVSSSELAKAS 184
 QY 159 IDLNIETIGMLOSOTQTEAFSSQLAKIGSTISQAKGFSNIGNKLOVL-NFSKTNIQLEI 217
 Db 185 IELINOLVDTVASLNNNVNFSQOLNLGSLVSTKHLNNGVAKLQNLPLMDINIGAGLDT 244
 QY 218 ITGLLSIGSGFALADKNASTGKVAAGFELSNQVIGNVTKAISVYLAQVAAGLSTTG 277
 Db 245 VSGILSAISAFSLSNADADTRTKAAGVGLTTLKVLGNVKGKISQYITIAQRAAGLSTSA 304
 QY 278 AVAALLTSSIMLAIISPLAFNADAKFHNANALDEPAKQKPFQYDGDHDLAETQKGVGTI 357

Db 305 AAGGLIASAVTLAISPLSLSLADKFRANKLEIYSQRKIKCIYODSLLAFFHKETGAI 364
 QY 338 EASLITTSIALCAVSAAGVAAVGAAPIALLVAGVTGLISGLEASRKQAMPESVANR 397
 Db 365 DASLTITSTVLASVSSGSLAAATTSILVGAAPVSAVAGVGLISGLEASRKQAMPESVANR 424
 QY 398 LQKILTEMKONGGONYPFKGYSRYAAVLANNLFLSLKELAEERVIATTOQRMDNN 457
 Db 425 MADVIAEMERKKA-GKNYFENGIDARHAAPLEDNEFKILSOYNEKSEVERSVLITQOHMDTL 483
 QY 458 IGLAGITKLGRIKSGNAYADAFEDGKKEVAG---SNITLDARTGIITISNSNGKKTQ 513
 Db 484 IGLAGVTFENGDKTSLGSKYIDYEEGRKLEKKPDEPKQVDPDLKGNIDLSDS--KST 541
 QY 514 ALHFTSPILTNGTERERITNKYITINKLFGKRVKNNQVTD-GEASSKLDPKVIQVRA 572
 Db 542 LKFTVPLTPEELERERQSGRYEYITELLVKGVDKTIVGVODKGAIVYDSNLIOHAS 601
 QY 573 ETEGT-DEIGLIVNKAAGNDIFVGGKMNIDGGDGHDRVFSK-DGGFNGITVDTGTSAT 630
 Db 602 VGNQYREIRIESHLGDDGDKVFLSAGSANTYAGGHVYITDKTIDY--LTIDGKTAT 659
 QY 631 EAGSYTVNRKVARGD--IYHEVVKROETKRTETIOYRDYELRKV-GYGYOSTDMLKS 687
 Db 660 EAGNTVTR-VLGGDVKVLQEVYKQEVYSGKREKTQYRSYFTIINGKMLTENDLYS 718
 QY 688 VEEVYISGFNDVFKSGFNDIFHSGEGDDLLDGGAGDOR----- 726
 Db 719 VEEILGTRAKRKFQSGKRTDIFHGADGDDLLTEGNDGNDRLYDKGNDTLGSGNGDDLYG 778
 QY 727 -----LFGKGNRLSGDEGDDLLDGGSG 750
 Db 779 GDGNDKLIGVANNYLNCGDDELDQVGNSLAKNVLFGKGNKLYGSEBADDLDGEG 838
 QY 751 DDVLNGAGNDVYIFRKGGNDLYDGTG--NDKLAFADANISDMIRTEGIIIVKEND- 808
 Db 839 DDLKGGYGNIDYRSLSGYGHITIDGKREKDLISLDIDFRDVAFRREGNDLIMYKGE 898
 QY 809 -----HSGSINIPWYITSNLQNYOSKNTDHIKIDOLGKDSYITTSODIKLIDCKD 860
 Db 899 NVLSIGHKNGITFRNWF-----EKESGDISHNELIQIFDKSGRIITDLSLKALEYQORN 953
 QY 861 -----DGTVITTSQ-----ELKRLADENKSGKLSASDIASSLNKLYGSMALFGT 903
 Db 954 NKASYVYGNDALAYSGDNLPLINEITSKISAGSPDYKEERTASLTLQSGNASDFSY 1013
 QY 904 A-NSVS 908
 Db 1014 GRNSTT 1019

RESULT 8
 hemolysin A - Escherichia coli
 C:Species: Escherichia coli
 C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 18-Jun-1999
 C:Accession: A24433; I41280
 R:Felelt, T.; Pellet, S.; Welch, R.A.
 J. Bacteriol. 163, 94-105, 1985
 A:Title: Nucleotide sequence of an Escherichia coli chromosomal hemolysin.
 A:Reference number: A24433; M0ID:85234404
 A:Accession: A24433
 A:Molecule type: DNA
 A:Residues: 1-1023 <FEU>
 A:Cross-references: GB:M10133; GB:M12863; NID:g146377; PIDN:AAA23975.1; PID:g146379
 A:Experimental source: GB:M10133, GB:M12863, NID:g146377, PIDN:AAA23975.1, PID:g146379
 R:Stanley, P.; Packman, L.C.; Kotonakis, V.; Hughes, C.
 Science 266, 1992-1996, 1994
 A:Title: Fatty acylation of two internal lysine residues required for the toxic activity
 A:Reference number: A53387; M0ID:95099325
 A:Contents: annotation; lysine palmitoylation
 A:Note: lysine modification is performed by the hlyc gene product

A:Residues: 17-42 <OH>
 A:Experimental source: strain 301-b
 A:Accession: PH0266
 A:Molecule type: protein
 A:Residues: 2-6, 'L', 8-26 <OH>
 C:Genetics:
 A:Gene: ltxA
 C:Function:
 A:Description: lyses human polymorphonuclear lymphocytes and monocytes
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: cytolysis; hemolysis; lipoprotein; periplasmic space; tandem repeat; thioles
 F:245-790/Domain: hemolysin A homology <HLYA>
 F:731-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIVF]-X)
 F:562,687/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 39.2%; Score 1820; DB 1; Length 1055;
 Best Local Similarity 40.3%; Pred. No. 1,4e-85;
 Matches 414; Conservative 185; Mismatches 298; Indels 130; Gaps 23;

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QY 3 NINIVKSNQAGLNSTKSGKLNLYAIKPKYDQKGTINDEIKADELGIARLAEPNH 62
DB 27 NIDAAEQLOKALDKLGKTKKLTLYIPKNY--KKNGITLALIKAAQKIGIEVHEGKDG 84
QY 63 TETAKSVDTVNOFLSTPOTGIAISATKLEKFLQ--KHSTNKLAGLGSVENIDKRLGA 120
DB 85 PALTNGILNTGKKLIGLTPRGILTFRPELDKNIQGNKHLNSVG---STGMLTFAIDV 140
QY 121 SNVLSTLSFLCTALAGLDSLIK--KGAAPDA-LAKASIDLINELIGNLSOSTOTI 176
DB 141 QSVLTLOAFMLNTAFSGMDLALIKARONGKNTVDTQAKASLNLINELIGTISSTNNV 200
QY 177 EAFSSQALAKGSTISOAKFSGNIGKLNQ---NFKSTNLGLIITGLSISGFLA 232
DB 201 DFFSQKLKGLALQOVKHFSGFKLKLPLKMLGK---GLGALSGVLSAISALLLA 257
QY 233 DKNASTGKKVAAGFELSNQVIGNVTKAISVYLAQVAVAGVAVAAALITSSIMLAIS 292
DB 238 NKDAOTAKAAAAAEELTKVGNIGKALTQYLIQAARAAAGLSTTPVAGLIASVSLAIS 317
QY 293 PLAFNNADKPFHNAALDEFAKQPFKEGYDDHLLAEYRGVGTIEASLTITSTALGAVS 352
DB 318 PLSEFLGIKOPDRARMLDEYSKRFKFGYNDLSLQGFYKNTGIADAITTINVLISAIA 377
QY 353 AGVSAVAAGSVAAPALVAVGTGLISGLEASQKAFESVAVANLQKTIEMEQONGQ 412
DB 378 AGVGAASAGSLVGAPITGLVSAITSLISGLIDASKQAVFEHIANOLADKIAMENKY-GK 436
QY 413 NYFDKGYDSRYAAYLANNLKFLSELNKLLEAERYIAITQQRWNNIGELAGITKIGERIK 472
DB 437 NYFENGVDARHSAFLEDSLKLFLNELREKYTENILSTIQQGMQDRIGLAGITNGDKIQ 496
QY 473 SGRVADAFEEGKVEYAGSN---ITLDAKGIIIDISNCKKQIALHFTSPLLTACTGES 528
DB 497 SGRAYVDYLKAGEELAKHSDKFTYOILDPKIGNIDLSGKSGST--LTFLNPLTAGKEE 554
QY 529 RERLTNGKYSYINKLKEFGRVANKMOVTDGEASSKL-DESKVIOR-VAETEGDELGIYNA 586
DB 555 RKTQSGKYEFTTELKAYKGRDMVKVCPNNSNGYDSSNLIQHAVTRDNKYLEARLANL 614
QY 587 KAGMDLFFVGGKMNIDGGGHDHREYFSKDGSGFNITVDGTSATGEASVYVNRKVARGI 646
DB 615 GAKDDYFVFGSGSTIVNAGDGYDVADYSK--CRTGALFTIDGRNNAKQAYVERDLSGIV 673
QY 647 YHEVYKROETVVGKRTFETIOYRDYEL--RKVGYGYOSTDNLKSYEETVGSOFNDVFGSK 704
DB 674 LQETVYSQOETKRGKAVYTDLELRYNKILDYIYYTNKGKHADELINSEYELTIGTLRDKFYGSK 733
QY 705 FNDIFHSGEGDDL-----LDGAGGDDRLF----- 728
DB 734 FNDVFHGHGDGDLTYGDDRLYGCGNGDEIHGGGQNDMLLYGAGAGNDRLFGEYGNMYLD 793
QY 729 -----GGKGNDRILSGDEGDDLLDGGSGDDVYLVNGAGANDVYIFRKGDG 770

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DB 794 GGRGDHLEHGNGSDILKRGSGNDKLFNGQGDLLDGGGEGDQLAGGEGNDIYVRKEYG 853
QY 771 NDTLYDGTGN-DKLAEPADANISDIMIERTKEGIYKRNDSGSINIPRYITSN-----LQ 825
DB 854 HHTITEHSGDKDKLSLANINLKDVSFERNGNDLLKTNRT-AVYFKMFSPKNSAGID 912
QY 826 NYO-----SNKTDHKIEQLIGKDGSYITSDQIDKTILODK 859
DB 913 EYORKLEYPKDRARLRKQFELORGKVDKSLNKNKVEIIGKDERITSDIDNLFPKFS 972
QY 860 KDGVIYTSQELKLU-ADENKSQKLSASDIAS-----LTKLVGSMALFETA-NS 906
DB 973 GKMKTISPEGLAGLILKKNCKSSSLMSRSSSMLTQKGLSNDISRTIISATVSGFSSGKA 1032
QY 907 VSSNALQ 913
DB 1033 LSASPLQ 1039
RESULT 10
139643
RXN-toxin I - Actinobacillus pleuropneumoniae
N:Alternate names: hemolysin Apxi
C:Species: Actinobacillus pleuropneumoniae
C:Date: 19-Jul-1996 #sequence revision 08-Nov-1996 #text_change 18-Jun-1999
C:Accession: I39643; S18769; S19645; S60732; S35781
R:Jansen, R.; Briatore, J.; Kamp, E.M.; Gielkens, A.L.; Smits, M.A.
Infect. Immun. 61, 3688-3695, 1993
A:Title: Structural analysis of the Actinobacillus pleuropneumoniae-RXN-toxin I (Apxi
A:Reference number: I39641; MUID:93366425
A:Accession: I39643
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-1022 <RES>
A:Cross-references: EMBL:X73117; NID:g312897; PIDN:CAA51548.1; PID:g312899
R:Frey, J.; Meier, R.; Gygis, D.; Nicolet, J.
Infect. Immun. 59, 3026-3032, 1991
A:Title: Nucleotide sequence of the hemolysin I gene from Actinobacillus pleuropneumo
A:Reference number: S18769; MUID:91348845
A:Accession: S18769
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-209, 'AMPYVTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <FRE>
A:Cross-references: EMBL:X52899; PIDN:g38949; PIDN:CAA37081.1; PID:g38950
R:Frey, J.; Heidmann, A.; Nicolet, J.; Boffin, A.; Prentki, P.
Gene 142, 97-102, 1994
A:Title: Sequence analysis and transcription of the apxi operon (hemolysin I) from Ac
A:Reference number: I39644; MUID:94237497
A:Accession: I39645
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-209, 'AMPYVTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <RE2>
A:Cross-references: EMBL:X68595; NID:g505568; PIDN:CAA46586.1; PID:g505570
R:Tacon, R.I.; Vazquez-Roland, J.A.; Gutierrez-Martin, C.B.; Rodriguez-Barbosa, I.;
MOL. Microbiol. 14, 207-210, 1994
A:Title: The RTX haemolysins Apxi and ApxiI are major virulence factors of the swine
A:Reference number: S60731; MUID:95131743
A:Accession: S60732
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 604-685 <TAS>
C:Comment: This organism causes porcine pleuropneumonia.
C:Genetics:
A:Gene: apxiA
C:Function:
A:Description: attacks blood cell membranes and causes cell lysis
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repe
F:443-789/Domain: hemolysin A homology <HLYA>
F:721-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIVF]-X)
F:560,686/Binding site: palmitate (lys) (covalent) #status predicted

```

Query Match 38.0%: Score 1767.5; DB 1; Length 1022;
 Best Local Similarity 40.1%: Pred. No. 6,8e-83; Indels 109; Gaps 26;
 Matches 401; Conservative 181; Mismatches 308;

8 KSNIOAGLNSTKSG-----KNLYLAIPKDYDPQKGTLPNFIKADELGIARLAEEP 60
 21 KSAKAGACALKNKGLQOVQAGOKLLIYIPKQOASTGSLNLYVAAELGIEVHREK 80
 61 NHTETAKSVYVNOFLSLTQTGIAISAVKLEFLQKHSTNKLAKGL-DSEVNIIDRLK 119
 81 NGTALAKLEFGTTEKLLGFSEGCIALFAPQFDKLKMN--QKLSKISGSSSEALGRLNK 138
 120 ASNVLSLTSFLGTALAGIELDLIK-----GGAAPDALAKASIDLINELIGLSOSTOT 175
 139 TOTALALOSFLGTALAGMDLRLRRRNGEVSSELAACAGVDLAADLVMIASATGT 198
 176 IEAFSSOLAKLGSTISOAKGFSNIGNKLOL-NFSKTNLGLTITGLSGISAGFALADK 234
 199 VDAFAQLGLKGNALSNTR-LSGLASKLNNLPDLISLAGPFDVSGILSVSASFILSNK 257
 235 NASTGKVAAGFELSNQVIGNVTKAISVYLAQVAAAGLSTTGAVAAALITSSIMLAISPL 294
 258 DADAGTKAAAGIETSKILGNICKAVSQYIIAQVAAAGLSTAAATGGLISVVALAISPL 317
 295 AFNNADKFNHANADEFKQFPGYDGHLLAEYQRGVTEASLTITSTALGAVSAG 354
 318 SFLNVADKFERAKOLEOYSERFKFGEGDLSLAFREYGALEALTTINVSLSAASAG 377
 355 VSAAGVAVGAPIALLVAGVTGLSIGLEPASKQAFESVANRLQGLLEMEKONGCONY 414
 378 VGAAATGSLVAGAVAAVVAITGIIISGILDASKAIFERATLANKIDMEKKH-GKNY 436
 415 FDKGYSRAVYLANNLKFLSELNKELEAERVIAITQQRMDNNGELAGITTKLGERIKS 474
 437 FENGYDARHSAFLIEDTFELLSQYNKESYERVAITQQRMDVNIIGELAGITRKGSPTK 496
 475 KAAVADPEOCKKYEAG-----SNITLDKNGIIDSNSNGKQALHTSPSLLAGTRESRE 530
 497 KAVYDFEERKLEKEDRDKKVPRLBEGKIDLSIN--KTYLLKLVTVTFVAGEITRE 554
 531 RLNGKSYINKLFGGVKNMAYTDEBASSKL-DEFSKIORVATEEGTDEIGLIVNAKAG 589
 555 RKOTGKEYTELFPVKGKEMVYTVGOSHAIYDTNLIOLALDKK-EKROYTIEBHLG 613
 590 --NDIIFVGGKMNIDGGDGHDRVYSK-DGFGNITVDGTSATEAGSYTVNKKV-ARGD 645
 614 EKMDRIYLSGSSSIYVAGNCHDAVYDKTDTGY--LTFDQSAQKAGEYIVTEKELKADVK 671
 646 IYHEVVKROTKYKRFETIQQYRDYELR--KVGYVOSTNMLKSVERTISQFNDPVKGS 703
 672 VLEVVAKTQDIISVKKSEKLEYRDYELSPRELNGIRAKELSHVEITISNKKRKFSGS 731
 704 KFNDFHSGED-----DLDDGAGDRLFGKGNDRSLSGEDDDL 745
 732 RFDIFPGAAGDEITGNDSHDLIGDDGNDVYHGGGNDHLVGGNNDLIGSKGNFL 791
 746 DGGSGDD-----VLNGAGANDY-----IFRKDDGNDTLVDTGND----- 781
 792 NGGDGDELOVFEQYVNLGAGANDILYSGDGTNLFDDGVGNDKIGYGLGKDIYRSKE 851
 782 -----KLAFDANI-----SDIMEERKEGIIVVRNDSG-SINIPR 817
 852 YGRHIIIEKGGDDTLILLSPDRDGFIRIGDILLVKKIIGGLYLYHEBYNGALATKD 911
 818 WYITSNLONYSNKTTHKIEBOLIGKDSYITSDQIDKILDDKKDGYITSOELKLADEN 877
 912 WF--KEKEGQN---KIKIYDKGACAYVLSQYLFELFAPGRINFPNGLEKLYYEG 965
 878 KSKRLASDIASSLUNKLVGSMALF-GTANSYSSNALOPT 915
 966 YN--ALPOLRKDIEOIIISSTGAFTGDHGVSVSGSGL 1001

RESULT 11

T00227

Hemolysin A toxin protein - Escherichia coli plasmid p0157

C:Species: Escherichia coli

C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000

C:Accession: T00227; T42148

R:Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, H.C.; Kube

S.; Shingawa, H.

DNA Res. 5, 1-9, 1998

A>Title: Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemor

A:Reference number: Z14127; M0ID:98290540

A:Accession: T00227

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-998 <MAY>

A:Cross-references: EMBL:AB011549; NID:94589740; PIDN:BA031774.1; PID:93337015

A:Experimental source: strain EHEC O157:H7, substrain RIMD 0509952

R:Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.

Nucleic Acids Res. 26, 4196-4204, 1998

A>Title: The complete DNA sequence and analysis of the large virulence plasmid of Esc

A:Reference number: Z22068; M0ID:98391744

A:Accession: T42148

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-998 <MAY>

A:Cross-references: EMBL:AF074613; PIDN:AC070116.1

A:Experimental source: strain EDL933; serotype O157:H7

C:Genetics:

A:Gene: hlyA

A:Genome: plasmid p0157

C:Superfamily: hemolysin A; hemolysin A homology

C:Keywords: cytotoxins; hemolysins; lipoprotein; toxin

F:233-776/Domain: hemolysin A homology <HLV>

F:550,675/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 37.7%: Score 1752; DB 2; Length 998;

Best Local Similarity 40.1%: Pred. No. 4.1e-82;

Matches 392; Conservative 177; Mismatches 307; Indels 102; Gaps 21;

8 KSNIOAGLNSTKSGKLNLYLAIPKDYDPQKGTLPNFIKADELGIARLAEEPNTETAK 67
 18 KSNFNTASSVSRSAGKLLILIPNTEAO-GVGNELVKADELGEIHRERBDTALN 76
 68 KSDVTNQLSLTQTGIAISATKLEFLQKHSTNKLAKGL-DSEVNIIDRLKAKSNVLS 126
 77 QFEGAERKVVGLTERGVAIFAPQLDKLOKY--QKVGSKIGGTAEVNGNMLGKAGTVLSA 134
 127 LSSFLGTALAGIELDLSLKK-----GGAAPDALAKASIDLINELIGNLSQSTQTEAFSSQ 182
 135 LQNTGTALSGMALDELRLKOREGEDISQNDIASSSTELNQVLVDVSSITVSDFSSQ 194
 183 LAKLSTISOAKGFSNIGNKLOL-NFSKTNLGLTITGLSGISAGFALADKNASTGK 241
 195 LNOGFSLSKPRLSVSGKQLNLPDLGRLGDVYSGILSAVSASPIIGNSDAHGTG 254
 242 VAAGFELSNQVIGNVTKAISVYLAQVAAAGLSTTGAVAAALITSSIMLAISPLAFMNAAD 301
 255 AAGIELTVOYLVGNVGAVSQYIIAQRMAOGLSTTAASAGLITSAVMALAIPLSFLAAD 314
 302 KFNHANADEFKQFPGYDGHLLAEYQRGVTEASLTITSTALGAVSAGVSAAG 361
 315 KFERAKOLEYSEKFKLNTNEDGLLAFHKEITAIDALTTINTVSSVAGVSAASSA 374
 362 SAVGAPIALLVAGVTGLSIGLEPASKQAFESVANRLQGLLEMEKONGCONYEDKGYDS 421
 375 SLIGAPISMLVSAATGTLISGILEASKQAMFEVHAEKFAARINWEKEH-GKNYPENGYDA 433
 422 RYAAVYLANNLKFLSELNKELEAERVIAITQQRMDNNGELAGITTKLGERIKSGAAYDAF 481
 434 RHAFLSDLSLTLADFSRQNHAVERAVALITQOHMDEKIGELAGITRNADRSQSKAAYINYL 493

C:Superfamily: cyclolysin; calmodulin-sensitive adenylate cyclase catalytic domain homol
 C:Keywords: tandem repeat
 F:15-338/Domain: calmodulin-sensitive adenylate cyclase catalytic domain homology <NDB>
 F:543-1084/Domain: hemolysin A homology <HLTA>

Query Match 17.4%; Score 809.5; DB 2; Length 1705;
 Best Local Similarity 27.8%; Pred. No. 1.9e-33;
 Matches 255; Conservative 137; Mismatches 333; Indels 193; Gaps 28;

106 GLDSVENIDRLKASNVLTSLSTFLGTALAGIELDLSL-----KKGDAP-----151
 403 GYSLDGV-----GSRFSLGEVSDMAAVEAELEMTROYLAGARODAEPCVSGASAHW 458
 152 -----DALAKASIDLNEIIGNSO-----STQT-IEAFSSQAKIG-----STI 190
 459 GORALOGAQAQVAAQORLVHAIALMTQFGRAGSTNTPQEAASLSAAVFGLEBASSAVAEIV 518
 191 S-----OAKGFSNIGKNLQNLNFSKTLNLEIITGLSGISAGFALADKNASTGKV 242
 519 SGFFRRSGRRMAGCGVAG-----GAMALGGGICAGVAGMSLTD-DAPAGOKA 564
 243 AAGFELSNOYIGVNTAKAISVYL-----AQRVAGLSTTGAVAAITSSIMLAISPLAFMN 298
 565 AAGAEIALQLTGTVELASSTIALAAARCVTSGLQVAGSAGAAALAAALSPMEIYG 624
 299 AADKFNANMLDEFAPKFRKFGYGDHLLAEYQGVCTIEASLTITSTALGAVSAGVSA 358
 625 LVQOSHAPADLDKLAQESSAAVEGEGDALLAQVLRDKTAABCAVAVAGSAVLTVAASVIA 684
 359 AVGSANGAPIALLVAGYTGILSGILEASKOAFESVANRLQGLKEWEKONGCONYFDKG 418
 685 AASVYCAPAVAVYVSLTGLANGILRGVQPIIEKLANDVARKI---DELGGPAYTEKN 741
 419 YDSRYAAYLANN--IKFSELNKELEAEVIAITQGRWNNIGELAGTYKGERISGK 475
 742 LQARH -EOLANSDELKRMKLDLQAGMNASVYGVQTEISKAELAITGNAHLNSAD 800
 476 AYDAFEDGKKEVSGSNITDAKTCIIDSNSGKTKQALHFTSPLLTAGHESREPLNG 535
 801 VFDPRFQGERV-AGQPVLDVAAGIDIASRKGR-PALFTTPLAAPGEQRRRTKYG 858
 536 KYSYINKLKE-GRVKNQVTDGEASRLDFSKVIQVVAETEGT--DEIGLIVNKAAGND 592
 859 KSEFTTVELVQKDRIRIDGADTTIDLAKVSQLVANGVLYKHSIKLEIVGDDGDDV 918
 593 IFWGQGMNIDGDDHVRVFSKDGFGENTVDGTSATFAGSYTVNKRKAVAGDIYHEVVK 652
 919 VLNASRHHYDGGAGTNTVSAAALGRDSDITV---SADGERFNVRRKQNNANAYREGVA 974
 653 ROETKVKRRTETIORYELRKVGYGOSTDNLSKVEEVIGSORNDVFKSGKFNDFHSG 712
 975 TQKTAAYKRTENVQYRHEVLARVGO-LVEYDTLEHVOHIIIGAGNDSTIGAHNPLAGC 1033
 713 EGDLDLGGAGDDLEFGKGNDRLSGDEGDDL-----DDGSG-----750
 1034 AGDRLDGGAGNDLTVGEBGHNTVVGAGDDVFLQDLGCVMSQDLGGAGVTVYKYNHQP 1093
 751 -----DDVL 754
 1094 SEERLERMGDTGIHADLOKGTVEKWPALNLFVYHVKNIENTHGSLSLNDSTIAGDDRDEL 1153
 755 NGAGNDVYIFRKGD-----GNDTLVDTGNDKRLAFADANISDIM-----IERTKEGI 802
 1154 WGHGNDLTHGRRDDLLRGGLGDTLYGEDGNDIFLQDDTVSDDDIDGAGLDTVDYAA 1213
 803 IVKRNDSGSIINIRWY---ITSNLOVQNSKTDHK-----IEOLIG---KDGSY 846
 1214 MI-----HAGNTVAPHEVGFGEADLSBGMVAKARRGHDYDVSRYENVNIGTSMKD-VL 1268
 847 ITSQDIDKILQDKKQGV 864
 1269 IGDAGANTLMGGGDDTV 1286

RESULT 14 OYBRC

Cyclolysin - Bordetella pertussis
 N:Alternate names: adenylate cyclase precursor; calmodulin-sensitive adenylate cyclase
 N:Contents: adenylate cyclase (EC 4.6.1.1), calmodulin-sensitive; hemolysin
 C:Species: Bordetella pertussis
 C:Date: 31-Dec-1990 #sequence,revision 31-Dec-1990 #text,change 16-Jul-1999
 C:Accession: S00893; S14100; S02389
 R:Glasier, P.; Ladant, D.; Sezer, O.; Pichot, F.; Ullmann, A.; Danchin, A.
 Mol. Microbiol. 2, 19-30, 1988
 A:Title: The calmodulin-sensitive adenylate cyclase of Bordetella pertussis: cloning
 A:Reference number: S00893; MUID:88216178
 A:Accession: S00893
 A:Molecule type: DNA
 A:Residues: 1-1706 <L>
 A:Cross-references: EMBL:Y00545; MID:g936665; PIDN:CAA68613.1; PID:g936666
 R:Glasier, P.; Sakamoto, H.; Bellalou, J.; Ullmann, A.; Danchin, A.
 EMBO J. 7, 3997-4004, 1988
 A:Title: Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase--haemoi
 A:Reference number: S02386; MUID:89091151
 A:Contents: annotation; Identification of adenylate cyclase--hemolysin bifunctional
 R:Munier, H.; Gilles, A.M.; Glasier, P.; Krin, E.; Danchin, A.; Sartati, R.; Barzu, O
 Eur. J. Biochem. 196, 469-474, 1991
 A:Title: Isolation and characterization of catalytic and calmodulin-binding domains
 A:Reference number: S14100; MUID:91177021
 A:Accession: S14100
 A:Molecule type: protein
 A:Residues: 1-78, 'M', 80, 'M', 82-97, 'M', 99-139, 'M', 141-178, 'M', 180-399 <MUN>
 R:Hackett, M.; Guo, L.; Shabanowitz, J.; Hunt, D.F.; Hewlett, E.L.
 Science 266, 433-435, 1994
 A:Title: Internal lysine palmitoylation in adenylate cyclase toxin from Bordetella p
 A:Reference number: A55167; MUID:95025937
 A:Contents: annotation; lysine palmitoylation
 A:Comment: B. pertussis, the etiological agent of whooping cough, disrupts mammalian
 action by host cell calmodulin of the adenylate cyclase activity of bacterial cycloly
 C:Comment: Adenylate cyclase activity is activated upon binding of calmodulin in the
 C:Genetics:
 A:Gene: cyaA; cya

C:Superfamily: cyclolysin; calmodulin-sensitive adenylate cyclase catalytic domain h
 C:Keywords: calcium binding; calmodulin binding; cAMP biosynthesis; carbon-oxygen ly
 F:15-338/Domain: calmodulin-sensitive adenylate cyclase catalytic domain homology <N
 F:25-35/Region: calmodulin binding #status predicted
 F:59-66/Region: nucleotide binding #status predicted
 F:544-1085/Domain: hemolysin A homology <HLTA>
 F:1033-1041,1042-1050,1174-1182,1289-1297,1298-1308,1316-1324,1430-1438,1556-1564/Re
 F:983/Binding site: palmitate (lys) (covalent) #status experimental

Query Match 17.3%; Score 806; DB 1; Length 1706;
 Best Local Similarity 27.2%; Pred. No. 2.8e-33;
 Matches 247; Conservative 142; Mismatches 346; Indels 174; Gaps 26;

106 GLDSVENIDRLKASNVLTSLSTFLGTALAGIELDLSL-----KKGDAP-----151
 403 GYSLDGV-----GSRFSLGEVSDMAAVEAELEMTROYLAGARODAEPCVSGASAHW 458
 152 -----DALAKA-----SIDLINEI-----IGNLSQTFTEAFSSQAKIGTISO-A 193
 459 GORALOGAQAQVAAQORLVHAIALMTQFGRAGSTNTPQEAASLSAAVFGLEBASSAVAEIV 518
 194 KGFNIGKNLQNLNFSKTLNLEIITGLSGISAGFALADNASTGKVAAGFELSNOVI 253
 519 SGFFR-GSSRRMAGCGVAGGAMALGGGTAAVVAGMSLTD-DAPAGQAAAAGAEIALDVT 576
 254 GNVTKAISVYL-----AQRVAGLSTTGAVAAITSSIMLAISPLAFNNAADKFNHANAL 309
 577 GGYVELASSTIALAAAGVTSGLQVAGASAGAAAGALAAALSPMEIYGLVQSHYADQL 636
 310 DEFAKQFRKFGYDGDHLLAEYQGVCTIEASLTITSTALGAVSAGVSAAGVAGAPIA 369
 637 DLAQESSAYVEGDDALLAQVLRDKTAABCAVAVAGSAVLTVAASVIAAASVVGABVA 696

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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:58:48 : Search time 75.59 Seconds
(without alignments)
20.572 Million cell updates/sec

Title: US-09-884-696-13
Perfect score: 77
Sequence: 1 FNDIFHSGEDDL 14

Scoring table:
BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_032802.*

1:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1980.DAT.*
2:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1981.DAT.*
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7:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1986.DAT.*
8:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1987.DAT.*
9:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1988.DAT.*
10:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1989.DAT.*
11:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1990.DAT.*
12:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1991.DAT.*
13:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1992.DAT.*
14:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1993.DAT.*
15:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1994.DAT.*
16:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1995.DAT.*
17:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1996.DAT.*
18:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1997.DAT.*
19:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1998.DAT.*
20:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1999.DAT.*
21:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA2000.DAT.*
22:	/SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	927	22	AA62110
2	58	75.3	1049	18	AAW22159
3	58	75.3	1049	21	AA51412
4	58	75.3	1244	15	AA54781
5	52	67.5	758	17	AA86998
6	49	63.6	127	16	AA76990
7	49	63.6	450	22	AA60437
8	49	63.6	608	22	AA60436
9	49	63.6	924	12	AA10889
10	49	63.6	924	14	AA42385
11	49	63.6	924	14	AA42380

12	49	63.6	924	14	AA42378	Recombinant leukot
13	49	63.6	926	12	AA14482	LKT352. Pasteurel
14	49	63.6	926	14	AA34545	Leukotoxin 352 pro
15	49	63.6	926	15	AA50291	Recombinant leukot
16	49	63.6	926	17	AAW03945	P. haemolytica tru
17	49	63.6	926	19	AAW79568	Leukotoxin 352 pol
18	49	63.6	936	14	AA34547	GnRH-leukotoxin ge
19	49	63.6	936	14	AA34546	Somatosatatin-leuko
20	49	63.6	951	14	AA34548	Rotavirus VP4-leuk
21	49	63.6	953	11	AA607167	105SD PRX protein
22	49	63.6	953	12	AA15159	Leukotoxin from P.
23	49	63.6	953	14	AA43865	Leukotoxin protein
24	49	63.6	953	15	AA60072	ptx protein of Pa
25	49	63.6	953	22	AA60438	Pasteurella haemol
26	49	63.6	977	17	AAW03942	LKT-GnRH protein f
27	49	63.6	977	19	AAW79569	LKT-GnRH chimeric
28	49	63.6	1022	18	AAW22152	Apixia protein. Ac
29	49	63.6	1022	21	AA51406	A. pleuropneumonia
30	49	63.6	1023	16	AA76991	LhaA (low homology
31	49	63.6	1069	15	AA52748	Bovine IFNgamma/LK
32	49	63.6	1069	18	AAW13867	Chimeric protein #
33	49	63.6	1069	21	AAW21074	Bovine gamma-IFN/P
34	49	63.6	1098	13	AAW22103	Bovine IL-2 - LKT
35	49	63.6	1098	15	AA52747	Bovine IL-2/LKT ch
36	49	63.6	1098	18	AAW13866	Chimeric protein #
37	49	63.6	1098	21	AAW21073	Bovine IL-2/Pasteu
38	49	63.6	1098	21	AAW12561	APPA hemolysin an
39	49	63.6	1098	21	AAW22156	APPA hemolysin an
40	49	63.6	1098	21	AAW22156	APPA hemolysin an
41	49	63.6	1098	21	AAW22156	APPA hemolysin an
42	49	63.6	1098	21	AAW22156	APPA hemolysin an
43	49	63.6	1098	21	AAW22156	APPA hemolysin an
44	49	63.6	1098	21	AAW22156	APPA hemolysin an
45	49	63.6	1098	21	AAW22156	APPA hemolysin an

ALIGNMENTS

RESULT 1	
AA62110	standard; Protein; 927 AA.
XX	
AC	AA62110:
XX	
DT	29-MAY-2001 (first entry)
XX	
DE	M. bovis Dalton 2d RTX toxin A subunit.
XX	
KW	Moraxella: antigen; Immune response; Infection; RTX toxin; vaccine;
KW	antibacterial; A subunit.
XX	
OS	Moraxella bovis.
XX	
PN	WO200116172-A1.
XX	
PD	08-MAR-2001.
XX	
XX	
PF	31-AUG-2000; 2000MO-AU01048.
XX	
PR	31-AUG-1999; 99AU-0002571.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
PA	(UYME) UNIV MELBOURNE.
PI	Farn J, Strugnell R, Tennent J;
XX	
DR	WPI: 2001-235092/24.
XX	
DR	N-PSDB; AAF57230.
XX	
PT	Novel Moraxella bovis antigen useful in compositions for raising immune
XX	response in an animal, has protease, lipase or hemolysin activity

PS Claim 26; Fig 5; 60pp; English.

CC The invention relates to new Moraxella bovis antigens and nucleic acid
 CC sequences encoding these antigenic polypeptides. The antigenic
 CC polypeptides and polynucleotides are useful for raising an immune
 CC response in an animal directed against Moraxella, preferably against
 CC M. bovis or M. catarrhalis, and for treating Moraxella infections. The
 CC present sequence represents the amino acid sequence of the A subunit of
 CC the RTX toxin from M. bovis Dalton 2d.

XX Sequence 927 AA;

Query Match

Best Local Similarity 100.0%; Score 77; DB 22; Length 927;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 FNDIFHSGEGDDL 14
 |||||
 Db 705 fndifhsgeddl 718

RESULT 2

AAW22159 ID AAW22159 standard; Protein; 1049 AA.

XX AC AAW22159;

DT 16-FEB-1998 (first entry)

DE AprXIIIB protein.

XX RTX toxin; aprXICA gene; aprXIBD gene; aprXIIABCD gene;
 KW repeat in toxins toxin; cell-associated RTX toxin; vaccine production;
 KW therapy; A. pleuropneumoniae infection; swine pleuropneumonia.

XX Actinobacillus pleuropneumoniae.

PN CA2170839-A.

PD 02-SEP-1996.

XX 01-MAR-1996; 96CA-2170839.

PF 01-MAR-1995; 95US-0396244.

PR 01-MAR-1995; 95US-0396244.

PA (UYGU-) UNIV GUELPH.

PI MacInnes J, Mallard B, Ricciatti P, Rosendal S;

DR WPI; 1997-245536/23.

DR N-PSDB; AAT73220.

XX Preparations of microorganisms producing cell-associated RTX toxins

PT -especially for production of vaccines against swine

PT pleuro-pneumonia

XX Disclosure; Pages 107-110; 151pp; English.

PS AAW22151-W22161 represent A. pleuropneumoniae RTX (repeat in toxins)

CC toxins. These sequence are encoded by the aprXICA, aprXIB, aprXIIAB, C, and

CC aprXIIABCD genes (see AAT73217-73220), and can be expressed by

CC microorganisms used in the preparations of the invention. The

CC preparations are bacterial preparations comprising one or more isolated

CC and purified strains of a microorganism that produces one or more RTX

CC toxins, where the strains have at least one cell-associated RTX toxin.

CC The preparations are used for production of vaccines for the prophylaxis

CC and treatment of infectious diseases caused by microorganisms that

CC produce RTX toxins, where the strains have been attenuated or

CC inactivated. The vaccines are preferably against Actinobacillus

CC pleuropneumoniae infection (swine pleuropneumonia). It has been found

CC that A. pleuropneumonia produces significant quantities of

CC cell-associated RTX toxins when cultured under certain conditions, and

CC that the whole-cell protein composition of the cultures corresponds to
 CC the whole-cell protein profiles obtained from cells recovered at
 CC necropsy from the pleural fluid of infected swine. Vaccination with a
 CC bacterin prepared from heat-inactivated cultures having significant
 CC quantities of cell-associated RTX toxins give significant protection of
 CC swine against challenge with homologous strains.

XX Sequence 1049 AA;

Query Match

Best Local Similarity 75.3%; Score 58; DB 18; Length 1049;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEGDDL 14
 |||||
 Db 747 fndifhsgeddl 760

RESULT 3

AAV51412 ID AAV51412 standard; protein; 1049 AA.

XX AC AAV51412;

DT 05-MAY-2000 (first entry)

DE A. pleuropneumoniae aprXIIA protein.

XX RTX toxin; vaccine; Repeats in Toxins; immunostimulatory; antimicrobial;

XX antiinflammatory; antiarthritic; antiabortive; treatment; pneumonia;

XX pleuropneumonia; septicemia; nephritis; arthritis; endocarditis;

XX shipping fever; abortion; whooping cough; sleepy foal disease; joint ill;

XX urinary infection; peritonitis; meningitis; gastroenteritis;

XX passive immunization; aprXIIA.

XX Actinobacillus pleuropneumoniae.

OS US6019984-A.

PN 01-FEB-2000.

PD 23-DEC-1996; 96US-0772270.

XX 01-MAR-1995; 95US-0396244.

PR 01-MAR-1995; 95US-0396244.

PA (UYGU-) UNIV GUELPH.

PI Mallard B, Rosendal S, MacInnes J, Ricciatti P;

DR WPI; 2000-146864/13.

DR N-PSDB; AAZ88587.

XX Bacterial preparation comprising microorganisms which produce a member

PT of the Repeats in Toxins (RTX) family, useful for treating swine

PT pleuropneumonia, arthritis in swine, shipping fever and abortion in

PT cattle, and sleepy foal disease -

XX Disclosure; Column 77-84; 96pp; English.

PS This invention describes a novel bacterial preparation (I) which

CC comprises one or more isolated and purified strain(s) of a microorganism,

CC cultured in tryptone yeast extract (TYE) broth, which produces one or

CC more RTX toxins (belonging to the family of toxins referred to as Repeats

CC in Toxins), where the strain(s) have at least one RTX toxin which is

CC cell-associated. The products of the invention have immunostimulatory,

CC antimicrobial, antiinflammatory, antiarthritic and antiabortive activity.

CC The bacterial preparation may be used as vaccines for the prophylaxis and

CC treatment of infectious diseases caused by strains of microorganisms

CC which produce one or more RTX toxins. The infectious diseases are swine

CC pleuropneumonia, pneumonia, septicemia, nephritis and arthritis in swine;

CC septicemia, nephritis, endocarditis and arthritis in piglets; shipping

CC fever and abortion in cattle; whooping cough, sleepy foal disease or

CC joint ill (purulent nephritis, arthritis) in foals; septicemia,
CC polyarthritis and abortion in horses; and urinary infections,
CC peritonitis, meningitis, and gastroenteritis. The bacterial preparations
CC may also be used to prepare antibodies which may be used as a means of
CC passive immunization. This sequence represents the Actinobacillus
CC pleuropneumoniae appiia protein described in the method of the
CC invention.

SO Sequence 1049 AA:

Query Match

Best Local Similarity 75.3%; Score 58; DB 21; Length 1049;
Best Local Similarity 71.4%; Pred. No. 0.18;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEDDLL 14
Db 747 frdIfhgadgdll 760

RESULT 4

AAR54781
ID AAR54781 standard; Protein; 1244 AA.

AC AAR54781;

DT 15-OCT-1994 (first entry)

DE Leukotoxin Appiia.

KW Leukotoxin; Appiia; pleuropneumonia; vaccine; diagnostic.

OS Actinobacillus pleuropneumoniae.

PH Key Location/Qualifiers

FT Domain

FT Domain /label= transmembrane domain

FT Domain /label= transmembrane domain

PN MO9409821-A.

PD 11-MAY-1994.

PF 04-NOV-1993; 93MO-US10500.

PR 05-NOV-1992; 92US-0972229.

PR 03-JUN-1993; 93US-0072285.

PA (CORR) CORNELL RES FOUND INC.

PI Chang Y;

DR WPI: 1994-167130/20.

DR N-PSDB; AA064827.

PT DNA encoding Actinobacillus pleuropneumoniae leukotoxin - used to

PS Disclosure: Fig 3; 65pp; English.

CC The Appiia gene having the sequence given in AA064827 was isolated

CC from phage lambda clones yfc 26-28 and yfc 31-32 of a genomic

CC library of A. pleuropneumoniae ser. 2. The gene encodes a novel

SO Sequence 1244 AA:

Query Match

75.3%; Score 58; DB 15; Length 1244;

Best Local Similarity 71.4%; Pred. No. 0.21;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEDDLL 14
Db 920 frdIfhgadgdll 933

RESULT 5

AAR86998
ID AAR86998 standard; Protein; 758 AA.

AC AAR86998;

DT 04-JUL-1996 (first entry)

DE Enterohaemorrhagic E. coli hlyA gene product.

KW Enterohaemorrhagic Escherichia coli; virulent; EHEC; O157:H7 serotype;

KW detection; probe; primer: hlyA gene; enterohaemorrhagic colitis;

KW haemolytic uremic syndrome; mesenteric adenitis.

OS Escherichia coli (enterohaemorrhagic).

PN US5475098-A.

PD 12-DEC-1995.

PF 14-JUN-1994; 94US-0258188.

PR 14-JUN-1994; 94US-0258188.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Hall RH, Xu JG;

DR WPI: 1996-048546/05.

DR N-PSDB; AAT08098.

PT Enterohaemorrhagic E. coli (EHEC) nucleic acid sequences - useful

PT for probe and primer design for sensitive and specific detection of

PS Claim 1; Columns 37-42; 32pp; English.

CC Enterohaemorrhagic E. coli (EHEC) associated with enterohaemorrhagic

CC colitis, haemolytic uremic syndrome and mesenteric adenitis have

CC been found to carry a hlyA gene and a hlyB gene, separated by an

CC intergenic region. The hlyA gene and the intergenic region are

CC absent from bacteria not associated with these diseases and so

CC provide a useful target for detecting EHEC pathogens, esp. O157:H7

CC serotype E. coli. The present sequence is that of the protein

SO Sequence 758 AA:

OY 1 FNDIFHSGEDDLL 14
Db 480 frdIfhgadgdyl 493

RESULT 6
AAR76990
ID AAR76990 standard; protein; 127 AA.

AC AAR76990;

DT 13-MAR-1996 (first entry)

XX Actinobacillus antigenic toxin repeat (RTX) region.
 XX RTX; repeat; vaccine; antigenic; immunisation; pneumonia;
 KW Apl disease.
 XX Actinobacillus pleuropneumoniae.
 XX
 FH Key Location/Qualifiers
 FT Region 1..127
 FT /Label= repeat region
 FT /note= "tandem repeat units of 9 amino acids"
 XX
 PN JF07138185-A.
 PD 30-MAY-1995.
 XX
 PF 23-JUN-1993; 93JP-0152264.
 XX
 PR 23-JUN-1993; 93JP-0152264.
 XX
 PA (NISK) NIPPON SEIBUTSU KAGAKU KENKYUSHO ZH.
 XX
 DR WPI; 1995-228639/30.
 XX
 XX A vaccine contg. a product of the lhaa gene as the active ingredient
 PT - for prophylaxis of Actinobacillus (Haemophilus) pleuropneumoniae
 PT infectious diseases.
 XX
 PS Claim 1; Page 8; 15pp; Japanese.
 XX
 CC AAR76990 represents a repeat region of the lhaa (low homology to appa)
 CC gene product which is a toxin component. The repeat region and full
 CC gene product are useful as the active ingredient in vaccines for the
 CC prophylaxis of Actinobacillus (Haemophilus) pleuropneumoniae
 CC infectious (Apl) diseases.
 CC
 XX
 SQ Sequence 127 AA;

Query Match 63.6%; Score 49; DB 16; Length 127;
 Best Local Similarity 66.7%; Pred. No. 0.62;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FNDIFHSGEGDD 12
 Db 15 ftdlfnhgkqdd 26
 RESULT 7
 ID AAE04637 standard; Protein; 450 AA.
 AC AAE04637;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Pasteurella haemolytica modified leukotoxin 50 (lkt50) protein.
 KW Leukotoxin 50; lkt50; respiratory disease; infection; therapy;
 KW immunostimulant; antibacterial; vaccine; transgenic plant;
 KW animal feed; mutant; muten.
 XX
 OS Pasteurella haemolytica.
 OS Synthetic.
 PN WO200144289-A2.
 PD 21-JUN-2001.
 XX
 PF 15-DEC-2000; 2000WO-CA01498.
 XX
 PR 17-DEC-1999; 99US-0172148.

XX (UYGU-) UNIV GUELPH OFFICE.
 PA
 XX
 PI Lo RYC, Shewen PE, Lee RWH, Hodgins D, Strommer JN;
 XX
 DR WPI; 2001-408470/43.
 DR N-PSDB; AAD08976.
 XX
 PT Modified leukotoxin polypeptide is useful in a vaccine to prevent or
 PT treat Mannheimia (Pasteurella) infection (particularly M. haemolytica
 PT infection), and disease associated with a leukotoxin, e.g., respiratory
 PT disease.
 XX
 PS Claim 4; Fig 12; 70pp; English.
 XX
 CC The present sequence is Pasteurella (Mannheimia) haemolytica
 CC modified leukotoxin-50 (lkt50) protein. The modification comprises
 CC the removal of amino acids within the hydrophobic transmembrane
 CC domain of a full length leukotoxin protein. Modified leukotoxin
 CC sequences are used in vaccines to treat or prevent diseases associated
 CC with leukotoxin, e.g., respiratory disease, and Mannheimia infection
 CC (particularly M. haemolytica infection). In addition, the vaccine
 CC is used to prepare a medicament. Furthermore, the plant transformed
 CC with modified leukotoxin sequences is fed to an animal such as a
 CC ruminant, to prevent or treat respiratory diseases.
 CC
 XX
 SQ Sequence 450 AA;

Query Match 63.6%; Score 49; DB 22; Length 450;
 Best Local Similarity 58.3%; Pred. No. 2.6;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 2 NDFHSGEGDDL 13
 Db 324 ndlhnhgkqdd 335
 RESULT 8
 ID AAE04636 standard; Protein; 608 AA.
 AC AAE04636;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Pasteurella haemolytica modified leukotoxin 66 (lkt66) protein.
 KW Leukotoxin 66; lkt66; respiratory disease; infection; therapy;
 KW immunostimulant; antibacterial; vaccine; transgenic plant;
 KW animal feed; mutant; muten.
 XX
 OS Pasteurella haemolytica.
 OS Synthetic.
 PN WO200144289-A2.
 PD 21-JUN-2001.
 XX
 PF 15-DEC-2000; 2000WO-CA01498.
 XX
 PR 17-DEC-1999; 99US-0172148.
 XX
 PA (UYGU-) UNIV GUELPH OFFICE.
 PA Lo RYC, Shewen PE, Lee RWH, Hodgins D, Strommer JN;
 DR WPI; 2001-408470/43.
 DR N-PSDB; AAD08975.
 XX
 PT Modified leukotoxin polypeptide is useful in a vaccine to prevent or
 PT treat Mannheimia (Pasteurella) infection (particularly M. haemolytica
 PT infection), and disease associated with a leukotoxin, e.g., respiratory

PT	disease.
XX	
PS	ClaIm 2; Fig 2; 70pp; English.
XX	
CC	The present sequence is Pasteurella (Mannheimia) haemolytica
CC	modified leukotoxin-66 (lkt66) protein. The modification comprises
CC	the removal of amino acids within the hydrophobic transmembrane
CC	domain of a full length leukotoxin protein. Modified leukotoxin
CC	sequences in vaccines to treat or prevent diseases associated
CC	with leukotoxin, e.g., respiratory disease, and Mannheimia infection
CC	(particularly M. haemolytica infection). In addition, the vaccine
CC	is used to prepare a medicament. Furthermore, the plant transformed
CC	with modified leukotoxin sequences is fed to an animal such as a
CC	ruminant, to prevent or treat respiratory diseases.
XX	
Sequence	608 AA:
XX	

Query Match	63.6%	Score 49	DB 22	Length 608
Best Local Similarity	58.3%	Pred. NO. 3.6		
Matches	7	Conservative	3	Mismatches 2; Indels 0; Gaps 0.
2 NDIHFSGEGDDL 13				
: : : :				
db 429 ndlhngskgddl 440				

XX	AAQ10889
ID	AAQ10889 standard; Protein; 924 AA.
XX	
AC	AAQ10889;
XX	
DT	11-APR-1991 (first entry)
XX	
DE	Leukotoxin 352 encoded by plasmid PAA352.
XX	
KMT	LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia
XX	
OS	Pasteurella haemolytica A1 strain B122.
XX	
PN	CA2014033-A.
XX	
PD	07-OCT-1990.
XX	
PF	06-APR-1990; 90CA-2014033.
XX	
PR	07-APR-1989; 89US-0335018.
XX	
PA	(UYSA-) UNIV SASKATCHEWAN.
XX	
PI	Acres SD, Babluk LA, Potter AA, Lawman MJP:
XX	
DR	WPI: 1991-000097/01.
DR	N-PSSB: AAQ10272.
XX	
PT	Pasteurella haemolytica proteins and genes - used for producing
PT	vaccines to protect animals esp. cattle from respiratory diseases
PT	e.g. pneumonia.
XX	
XS	Claim 13; Fig 5; 87pp; English.
XX	
CC	Plasmid PAA352 is derived from PAA114, a clone isolated from a
CC	genomic library of P. haemolytica. The protein, designated "new
CC	leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin.
CC	LKT 352 and pref. antigenic fragments of it, can be used in
CC	vaccines to protect cattle from respiratory diseases. They can also
CC	be used to produce antibodies for immunoadfinity purificn. of
CC	further proteins. [Fig. contg. sequence v. poor]
XX	See also AAQ10890, AAQ10909, AAQ10910 and AAQ10783.
XX	
Sequence	924 AA;
SD	

	Query Match	Similarity	Score 49:	DB 12:	Length 924:
	Best Local	58.3%	Pred. No. 5.7:		
Matches	7:	Conservative	3:	Mismatches	2: Indels
					Gaps 0:
QY	2	NDIFHSGECDL	13		
	11:	11:1111:			
Db	745	ndllngkgyddl	756		

RESULT 10
AAR42385

XX
AC AAR42385;

DT 19-APR-1994 (first entry)

DE Recombinant leukotoxin peptide from plasmid pCRR28.

KW Haemophilus somnus; immunogenic; haemolysin; LppB, LppC;
KW thromboembolic meningoencephalitis; septicæmia; arthritis;
KW pneumonia; Ikta gene; haemin-binding protein; fuston protein.

05 *Pasteurella haemolytica*.

PN W09321323-A.

PD 28-OCT-1993.

PF 05-APR-1993; 93WO-CA00135.

PR 09-APR-1992; 92US-0865050.

PR 04-JUN-1992; 92US-0893426.

PR 29-MAR-1993; 93US-0038288.

XX

XX

PI Rioux C, Theisen M;

DR WPI; 1993-351733/44.

XX

PT selected from haemin-binding

XX

XX

CC Pasteurella haemolytica leuk

used in vaccines for prevention

CC and pneumonia in vertebrates

[illegible]

Query Match	63.68;
Post Local Similarity	69.38;

Matches 7; conservative

QY 2 NDI FHS GEGDDL 13

Db 747 ndl1hgkgddl 758

xx	RESULT	11
ID	AAR42380	standard; Protein; 924 AA.
xx		
AC	AAR42378	
DT	19-APR-1994	(first entry)
xx		
DE	Recombinant leukotoxin peptide (split) from plasmid pCCH4.	
xx		
KW	Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;	
KW	thromboembolic meningencephalitis; septicæmia; arthritis;	
KW	pneumonia; Ikta gene; haemin-binding protein; fusion protein.	
xx		
OS	Pasteurella haemolytica.	
xx		
PN	MO9321323-A.	
PD	28-OCT-1993.	
xx		
PF	05-APR-1993; 93WO-CA00135.	
xx		
PR	09-APR-1992; 92US-0865050.	
PR	04-JUN-1992; 92US-0893424.	
PR	04-JUN-1992; 92US-0893426.	
PR	29-MAR-1993; 93US-0038287.	
PR	29-MAR-1993; 93US-0038288.	
PR	29-MAR-1993; 93US-0038719.	
xx		
PA	(UYSA-) UNIV SASKATCHEWAN.	
xx		
PL	Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;	
PI	Roux C, Theisen M;	
xx		
DR	WPI; 1993-351733/44.	
xx	N-PSDB; AAO51082.	
PT	Haemophilus somnus immunogenic proteins used in vaccines -	
PT	selected from haemin-binding protein, haemolysin, LppB and LppC,	
PT	and corresp. DNA	
xx		
PS	Disclosure; Fig 6; 11pp; English.	
xx		
CC	The hmb gene encoding the haemin-binding protein was expressed in	
CC	E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene	
CC	Ikta coded for by plasmid pAA352. The hmb gene fragment was taken	
CC	from PRAP504 and starts at the codon for the 33 rd amino acid residue	
CC	of ORF1. The haemin binding protein can be used in vaccines for	
CC	preventing or treating H. somnus infections, which cause thromboembolic	
CC	meningo-encephalitis, septicaemia, arthritis and pneumonia in	
CC	vertebrates	
CC	See also AAR42370-86.	
xx		
SQ	Sequence 924 AA;	
xx		
QY	Query Match	63.6%; Score 49; DB 14; Length 924;
	Best Local Similarity	58.3%; Pred. No. 5.7;
Matches	7; Conservative	3; Mismatches 2; Indels 0; Gaps 0;
Db	2 NDIHSGEGDDL 13	
	: : :	
	747 ndllhgkgddl 758	
xx		
RESULT	12	
ID	AAR42378	
xx	AAR42378 standard; Protein; 924 AA.	
AC	AAR42378;	
DT	19-APR-1994	(first entry)
xx		

DE	Recombinant leukotoxin peptide (split) from plasmid pCCH5.
XX	
KW	Haemophilus somnus; immunogenic; haemolysin; lppB, lppC;
KM	thromboembolic meningococcal septicemia; arthritis;
KM	pneumonia; lktA gene; haemin-binding protein; fusion protein.
XX	
OS	Pasteurella haemolytica.
XX	
PN	WO9321323-A.
XX	
PD	28-OCT-1993.
XX	
PF	05-APR-1993; 93WO-CA00135.
XX	
PR	09-APR-1992; 92US-0865050.
PR	04-JUN-1992; 92US-0893424.
PR	04-JUN-1992; 92US-0893426.
PR	29-MAR-1993; 93US-0038287.
PR	29-MAR-1993; 93US-0038288.
PR	29-MAR-1993; 93US-0038719.
XX	
PA	(UYSA-) UNIV SASKATCHEWAN.
PI	Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
PI	Rioux C, Theisen M;
XX	
DR	WPI; 1993-351733/44.
DR	N-PSDB; AAO51081.
XX	
PT	Haemophilus somnus immunogenic proteins used in vaccines -
PT	selected from haemin-binding protein, haemolysin, lppB and lppC,
PT	and corresp. DNA
XX	
PS	Disclosure; Fig 5; 119pp; English.
XX	
CC	The hmb gene encoding the haemin-binding protein was expressed in
CC	E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene
CC	lktA coded for by plasmid pAA352. The hmb gene fragment was taken
CC	from pAA352 and starts at the codon for the third amino acid residue
CC	of ORF1. The haemin binding protein can be used in vaccines for
CC	preventing or treating H. somnus infections, which cause thromboembolic
CC	meningo-encephalitis, septicemia, arthritis and pneumonia in
CC	vertebrates.
CC	See also AAR42370-86.
XX	
XX	Sequence 924 AA:
SQ	
Query Match	63.6%; Score 49; DB 14; Length 924;
Best Local Similarity	58.3%; Pred. No. 5.7;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0.	
OY	2 NDIHSGEGDDL 13
	: :
Db	747 ndlhgkgyddi 758
RESULT 13	
1D	AAR14482 standard; Protein; 926 AA.
XX	
AC	AAR14482;
XX	
DT	15-JAN-1992 (first entry)
XX	
DE	LKT352.
XX	
KW	Antigen; leukotoxin; vaccine; lktA.
XX	
OS	Pasteurella haemolytica.
XX	
PN	WO9115237-A.
XX	

PD 17-OCT-1991.
 XX
 PF 17-OCT-1991; 91WO-CA00170.
 XX
 PR 05-APR-1990; 90US-0504850.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Acres SD, Barluk LA, Potter AA, Lawman MJP;
 DR WPI; 1991-324967/44.
 XX
 PT Vaccines for Pasteurella haemolytica infection in cattle -
 PT comprise sub-unit antigens from P haemolytica fibrinogen protein,
 PT plasmin receptor, 50 K outer membrane protein and leukotoxin.
 XX
 PS Disclosure; Fig 5; 92pp; English.
 XX
 CC LKT352 is 98% homologous with authentic leukotoxin and migrates
 CC to the same position on gels.
 CC The LKT352 gene was prepared as follows: Ikta, an MaeI fragment
 CC contg. the gene was ligated into the SmaI site of pUC13 to form
 CC pAI179. From this, two constructs were made in the pTac-based
 CC vector, pGH432:laci digested with SmaI. One, pAA342, consisted of
 CC the 5' AhairII fragment from Ikta while the other, pAA345, contained
 CC the entire MaeI fragment. Clone pAA342 expressed a truncated
 CC leukotoxin peptide at high levels while pAA345 expressed full
 CC length leukotoxin at very low levels. The 3' end of the Ikta gene
 CC of pAA345 was therefore ligated to StyI/BamHI digested pAA342 to
 CC yield pAA352 contg. the LKT352 sequence. The protein expressed
 CC from the vector can be used to prepare a subunit vaccine with
 CC other P. haemolytica antigens, e.g. fibrinogen protein, plasmin
 CC receptor or 50K outer membrane protein. The vaccines can be used
 CC to protect cattle from respiratory diseases such as pneumonia, esp.
 CC Shipping fever pneumonia.
 CC See also AAR14481, 83, 84 and 85.
 XX
 CC Sequence 926 AA;
 SO

Query Match 63.6%; Score 49; DB 12; Length 926;
 Best Local Similarity 58.3%; Pred. No. 5.7;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIRHSGEGDDL 13
 ||:|:|:|:|:
 Db 747 ndlhgkgddl 758

RESULT 14
 AAR34545
 ID AAR34545 standard; Protein: 926 AA.
 XX
 AC AAR34545;
 XX
 DT 23-AUG-1993 (first entry)
 XX
 DE Leukotoxin 352 produced from pAA352.
 XX
 KW Vector; LKT 352; flanking; recombinant; antigen; somatostatin;
 KW gonadotropin releasing hormone; rotavirus viral protein 4;
 KW carrier protein; lactation; reproduction.
 XX
 OS Pasteurella haemolytica.
 XX
 PN WO9308290-A.
 XX
 PD 29-APR-1993.
 XX
 PF 15-OCT-1992; 92WO-CA00449.
 XX
 PR 16-OCT-1991; 91US-0779171.
 PR 14-OCT-1992; 92US-0960932.
 PR

XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Hughes HPA, Potter AA, Redmond MJ;
 XX
 DR WPI; 1993-152482/18.
 DR N-PSDB; AAQ41317.
 XX
 PT Immunological carrier system with enhanced immunogenicity -
 PT comprises chimeric protein comprising leucotoxin peptide or
 PT homologous protein fused to antigen esp. somatostatin or
 PT gonadotropin releasing hormone
 XX
 PS Disclosure; Fig 3; 95pp; English.
 XX
 CC Gene libraries of P. haemolytica A1 (strain B122) were constructed
 CC in lambda gtlI and pUC13. Resulting clones were used to transform E.
 CC coli and individual colonies were pooled and screened for reaction
 CC with serum from a calf which had survived a P. haemolytica infection
 CC and that had been boosted with a conc. culture supernatant of P.
 CC haemolytica to increase anti-leukotoxin antibody levels. Positive
 CC colonies were screened for their ability to produce leukotoxin by
 CC incubating cell lysates with bovine neutrophils and measuring the
 CC release of lactate dehydrogenase from the neutrophils. A 4kb
 CC fragment was obt'd. Progressively larger clones were isolated by
 CC chromosome walking to isolate full length recombinants of ca. 8kb,
 CC in pAI14. The clone was subjected to restriction enzyme digestion
 CC to yield two clones, one expressing truncated leukotoxin peptide at
 CC high levels and the other expressing the full length leukotoxin at
 CC low levels. The 3' end of the Ikta gene from the full length clone
 CC was ligated to the truncated gene clone to yield plasmid pAA352. The
 CC clone was used to produce chimeric proteins by gene fusion with an
 CC antigen coding sequence, e.g. the coding sequence of somatostatin,
 CC gonadotropin releasing hormone or rotavirus viral protein 4, i.e.
 CC leukotoxin works as a carrier protein to bring about a larger
 CC immune response than the antigen alone. Immunisation with these
 CC antigens can regulate growth rate, lactation and reproductive
 CC efficiency. See also AAR34546-8.
 XX
 CC Sequence 926 AA;
 SO

Query Match 63.6%; Score 49; DB 14; Length 926;
 Best Local Similarity 58.3%; Pred. No. 5.7;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIRHSGEGDDL 13
 ||:|:|:|:|:
 Db 747 ndlhgkgddl 758

RESULT 15
 AAR50291
 ID AAR50291 standard; Protein: 926 AA.
 XX
 AC AAR50291;
 XX
 DT 06-OCT-1994 (first entry)
 XX
 DE Recombinant leukotoxin from plasmid pAA352.
 XX
 KW Vaccine; outer membrane protein; OMP; Haemophilus somnus;
 KW iron regulated protein; leukotoxin; Pasteurella haemolytica;
 KW LKT352.
 XX
 OS Pasteurella haemolytica A1 (strain B122).
 XX
 PN CA2099707-A.
 XX
 PD 03-JAN-1994.
 XX
 PF 29-JUN-1993; 93CA-2099707.
 XX

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OM nucleic - nucleic search, using sw model

Run on: September 15, 2002, 09:00:42 : Search time 433.33 Seconds
(without alignments)
11030.600 Million cell updates/sec

Title: US-09-884-696-1

Perfect score: 2784

Sequence: 1 atgtccaataataatgtaat.....tttggtccaagtgttag 2784

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N.GeneSeq_032802:*

- 1: /SIDS1/gcgdata/geneSeq/geneSeqn-emb1/NA1980.DAT:*
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- 4: /SIDS1/gcgdata/geneSeq/geneSeqn-emb1/NA1983.DAT:*
- 5: /SIDS1/gcgdata/geneSeq/geneSeqn-emb1/NA1984.DAT:*
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- 22: /SIDS1/gcgdata/geneSeq/geneSeqn-emb1/NA2001A.DAT:*
- 23: /SIDS1/gcgdata/geneSeq/geneSeqn-emb1/NA2001B.DAT:*
- 24: /SIDS1/gcgdata/geneSeq/geneSeqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2782.4	99.9	3231	22	AAF57290
2	817.6	29.4	2788	12	AAO10727
3	815.6	29.3	3311	18	AAT60032
4	815.6	29.3	3311	21	AAAT2483
5	815	29.3	2817	14	AAO41322
6	815	29.3	2861	14	AAO41323
7	814.4	29.3	2794	12	AAO14238
8	814.4	29.3	2794	14	AAO41317
9	814.4	29.3	2794	15	AAO44760

10	814.4	29.3	2794	19	AAV61530
11	814.4	29.3	2934	17	AAT37176
12	814.4	29.3	2934	19	AAV61531
13	814.4	29.3	3229	15	AAO34213
14	814.4	29.3	3229	18	AAAT60033
15	814.4	29.3	3229	21	AAAT72484
16	814.4	29.3	3646	14	AAO51086
17	814.4	29.3	3887	14	AAO51082
18	814.4	29.3	3977	14	AAO51081
19	814	29.2	3311	13	AAO22771
20	814	29.2	3311	15	AAO54212
21	814	29.2	3879	14	AAO64610
22	814	29.2	7184	15	AAO70050
23	813	29.2	7183	11	AAO6074
24	812.8	29.2	3838	14	AAO41321
25	811.2	29.1	2794	17	AAT37179
26	807.6	29.0	4203	12	AAO45000
27	800.4	28.8	3848	17	AAT45417
28	775	27.8	4731	18	AAT73219
29	775	27.8	4731	21	AAZ88586
30	773.4	27.8	3831	12	AAO11873
31	629	22.6	4008	15	AAO64827
32	629	22.6	7721	18	AAT73220
33	629	22.6	7721	21	AAZ88587
34	488.8	17.6	3762	18	AAT73217
35	488.8	17.6	3762	21	AAZ88584
36	473.8	17.0	1827	22	AAO89975
37	466.2	16.7	3072	16	AAO94783
38	466.2	16.7	3240	16	AAO94784
39	403	14.5	2278	17	AAT08098
40	371.2	13.3	1359	22	AAO89976
41	343.2	12.3	2088	19	AAV61535
42	343.2	12.3	2088	21	AAZ55700
43	343.2	12.3	2088	21	AAZ46400
44	342.4	12.3	1473	20	AAV99361
45	341.8	12.3	1635	19	AAV61532

ALIGNMENTS

RESULT 1	AAF57290	standard: DNA: 3231 BP.
ID	AAF57290	
XX	AAF57290;	
AC	AAF57290;	
XX		
XX	29-MAY-2001 (first entry)	
DT		
XX		
DE	M. bovis Dalton 2d RTX toxin A subunit encoding DNA.	
XX		
KW	Moraxella; antigen; Immune response; Infection; RTX toxin; vaccine; antibacterial; ds.	
KW		
XX		
OS	Moraxella bovis.	
XX		
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FT	CDS	1..195
FT		/*tag= b
FT		/note= "partial coding region of RTX toxin C subunit"
FT	CDS	3080..3250
FT		/*tag= c
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PD	08-MAR-2001.	
XX		
XX	31-AUG-2000; 2000WO-AU01048.	
XX		

Nucleic acid encod
LRT-GNR fusion of
Nucleic acid encod
Bovine IFNgamma/LK
Chimeric protein #
Bovine gamma-IFN/P
Plasmid pCRR28 whi
Plasmid pCRR28 whi
Plasmid pCRR28 whi
Bovine IL-2 - LRT
Bovine IL-2/LRT ch
Leukotoxin genes h
px gene of Pasteu
Sequence encoding
Somatostatin-leuko
P. haemolytica leu
Leukotoxin genes.
P. suis leukotoxin
ApixiAB/C gene. A
A. pleuropneumonia
apPCA region encod
Leukotoxin ApixiA
ApixiIABCD gene.
A. pleuropneumonia
ApixiA gene. Acti
A. pleuropneumonia
Pasteurella haemol
Lina (low homology
Lina (low homology
Enterohaemorrhagic
Pasteurella haemol
Nucleic acid encod
DNA encoding a leu
conatoxin relae
Leukotoxin carrier
Nucleic acid encod

PR 31-AUG-1999. 99AU-0002571.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (UYME) UNIV MELBOURNE.
XX Farn J, Strugnelli R, Tennent J;
XX WPI: 2001-225092/24.
DR P-SDB; AAB62110, AAB62112, AAB62113.
XX Novel Moraxella bovis antigen useful in compositions for raising immune
PT response in an animal, has protease, lipase or hemolysin activity -
PS Claim 32, Fig 5; 60pp; English.
XX The invention relates to new Moraxella bovis antigens and nucleic acid
CC sequences encoding these antigenic polypeptides. The antigenic
CC polypeptides and polynucleotides are useful for raising an immune
CC response in an animal directed against Moraxella, preferably against
CC M. bovis or M. catarrhalis, and for treating Moraxella infections. The
CC present sequence represents the nucleotide sequence of the A subunit of
CC the RTX toxin from M. bovis Dalton 2d.
XX
XX
SQ Sequence 3231 BP; 1072 A; 478 C; 671 G; 1010 T; 0 other;

Query Match 99.9%; Score 2782.4; DB 22; Length 3231;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 292 ggaataaaatcttacttgcgtatcccaagaattatgctcgcaaaaagtgagact 351
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DB 352 ttaattgtttatgaagcgtcgaatgaatgaatgctgcttgaagcaagcgt 411
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DB 832 aacaagtgtcaaaacttaatttttctaaanaaatcttggtttggaataattactggt 891

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QY 2401 ggtatatagtttaaagaagaatgatacttcaagttagtataacataccagaatggtacata 2460
DB 2632 ggtatatagtttaaagaagaatgatacttcaagttagtataacataccagaatggtacata 2691
QY 2461 acatcaaatctcaaaatattcaaaatgataaagaatcacaataaattgagcaactaatt 2520
DB 2692 acatcaaatctcaaaatattcaaaatgataaagaatcacaataaattgagcaactaatt 2751
QY 2521 ggtaaagatgtagtatactacttccgaatccaattgataaaaatttgcgaagataagaa 2580
DB 2752 ggtaaagatgtagtatactacttccgaatccaattgataaaaatttgcgaagataagaa 2811
QY 2581 gatgtgacagtaatactcacaagaatgtaaaagctgtgtagatgaataagagcaca 2640
DB 2812 gatgtgacagtaatactcacaagaatgtaaaagctgtgtagatgaataagagcaca 2871
QY 2641 aaattctcgcttcgacacttgcgaatgagcttaataaagctgtgtggtcgaatgacata 2700
DB 2872 aaattctcgcttcgacacttgcgaatgagcttaataaagctgtgtggtcgaatgacata 2931
QY 2701 ttgtgtagcagcaaatagtgtagtcttaacgcttacaacgaatctacaacgaactaca 2760
DB 2932 ttgtgtagcagcaaatagtgtagtcttaacgcttacaacgaatctacaacgaactaca 2991
QY 2761 ggaatttggctccaaagtgttag 2784
DB 2992 ggaatttggctccaaagtgttag 3015

RESULT 2
AAQ10727
ID AAQ10727 standard; DNA; 2788 BP.
XX
AC AAQ10727;
XX
DT 11-APR-1991 (first entry)
XX
DE Leukotoxin 352 gene in plasmid pAA352.
XX
KW LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia;
KW ds.
XX
OS Pasteurella haemolytica A1 strain B122.
XX
PN CA2014033-A.
XX
PD 07-OCT-1990.
XX
PE 06-APR-1990; 90CA-2014033.
XX
PR 07-APR-1989; 89US-0335018.
XX
PA (U95A-) UNIV SASRATCHEMAN.
XX
PI Acres SD, Babiuk LA, Potter AA, Lawman MJP;
DR WPI, 1991-000097/01.
DR P-PSDB; AAR10889.
XX
PT Pasteurella haemolytica proteins and genes - used for producing
PT vaccines to protect animals esp. cattle from respiratory diseases
PT e.g. pneumonia.
XX
PS Claim 13; Fig 5; 87pp; English.
XX
CC Plasmid pAA352 is derived from pAA114, a clone isolated from a
CC genomic library of P. haemolytica. The protein encoded by the
CC plasmid, "new leukotoxin" or "LKT 352" is 98% homologous to
CC authentic leukotoxin. LKT 352 and pref. antigenic fragments of it,
CC can be used in vaccines to protect cattle from respiratory diseases.
CC They can also be used to produce antibodies for immunofluorescence
CC purification of further proteins. [Fig. contg. sequence v. poor]
CC See also AAR10890, AAR20909, AAR10910 and AAQ10783.
XX
SQ Sequence 2788 BP; 928 A; 487 C; 597 G; 776 T; 0 other;

Query Match 29.4%; Score 817.6; DB 12; Length 2788;
Best Local Similarity 60.0%; Pred. No. 3,5e-171;
Matches 1530; Conservative 0; Mismatches 964; Indels 54; Gaps 8;

QY 53 caaagcttgatlaaanaaacttacttctgcatcccaaaatatagtccgcaaaaag 112
DB 29 caaaacttggggcaaaaaaataatcattctctatactccccaataatcacaatgtactg 88
QY 113 gttggacttlaaagatttataaagctgtgataatgagtagtattgtctgttagcag 172
DB 89 aacaagatttacaagatttagtcaaaagcggcgaaggttgggattgggtacaaaag 148
QY 173 aagagcttaatacacttgaaacagcaaaaaaactcgttgacacagtaatacgtttctc 232
DB 149 aagaacgcaataatattgaaacagctcaaacagtttagcagattccaacgctattg 208
QY 233 cctcacaacaaactgtattcttctgcaacaacaaattgaagaagtcttacaacaaac 292
DB 209 gcttaactgtagtggtgattgtgtatccgctccacaacaaattgataatgtcaccagaa- 267
QY 293 attctacaataagtagccaaggttagacagtgtagaanaataattgactgtaaatag 352
DB 268 -----actaaagcaagccaagcattaggttctgcgcaagcaactgtgtaacaaatgcaa 319
QY 353 gtaaaagcaagtaatgatatatacaacataagctcttttttggcactgcatagcggta 412

Db 320 ataaagcaaaactgatatcttgcgcatcaaatctatttagagctcagcttcttgctgaa 379
Qy 413 tagaacttgattctttaatacaaaaagtgatgctgacccgtatgcttgctgaaagcta 472
Db 380 tgaattatgatgagccttaccagaa----taacgcaacccaacatgctcttgctaaagctg 436
Qy 473 gtaattgacttgatataagataatggttaatactatactcagagtaactcaaaagatgaa 532
Db 437 gcttgagagctaaccaattcttaattgaaatattgtaattcagtaaaacacttgacg 496
Qy 533 catttcttcacggttagcaaaagttaggttctctctatatcgcgcggtcaaaagccttcccta 592
Db 497 aatttgctgagcaaatatagtcgaattcttgctcaaaacatacaaaatacaaaagctlaagga 556
Qy 593 atataaggaacaagtgccaacacttaaat---tttcttaaaacaacatcttgcttgaa 649
Db 557 ctttagagagcaaacatacaaaaataatcggtgacttgataaagcgtcgtctggttagatg 616
Qy 650 taattactgtgtgctatcaggaatcttcgcagccttgctttagcggaataaaatgcata 709
Db 617 ttactcaggagctatlatcggcgcaaacagctgcacttgacttgacagataaaatgctt 676
Qy 710 cgaactggcaaaaagttgctgcagagtttgtaattagaacaatcaagttatgtaattgaa 769
Db 677 caacagctataaaaagtggtgctgaggttttgtaattgcaaaccaaggtctggttaactta 736
Qy 770 caaaagcaattcttcatalatggttttagacaacggtgtgctgctgctgctatacaactatg 829
Db 737 ccaaaagcgtttctcttaacttttagccaacggtgtgcaagcaggttattcttcaactg 796
Qy 830 gtgctgtgtgctgttataacttactcatcgattatggtgcaattagtccttggcattta 889
Db 797 ggcctgtgctgcttlaattgcttactgcttctctctgcatgaagccatlaagcatttg 856
Qy 890 tgaatgacagagataaattcaatcatgctatgctctgtagttagttgcaaaaacttcc 949
Db 857 ccggtatctgcgataaattcaatcatgcaaaaagtttagagagttatgcccgaacgcttta 916
Qy 950 gaaatttgctatgatagtagggatcatcttattctgctgaatacaagcgtggtgtggttacta 1009
Db 917 aaaattagagctatgacggagataattattatagcagaatalcagcggggaacagagacta 976
Qy 1010 ttgaagcttcaataacacaaatagtaagcagcataggttcctcgtggttcccg 1069
Db 977 ttgatttgatcggttactgcacataatlaacgcgcatgycgcgtatgctggtgtgtctg 1036
Qy 1070 ctgctgtgttagagatcgctggtgtgtgacccgagattgacattatgctgcaggtgttca 1129
Db 1037 ctgctgtagccgctcgtggttattgcttcacccgattgctcttaattagttatccggtattac 1096
Qy 1130 gatgtactctggaattttagaagcgtlctaaacagagcaatggttgaagtgtgtctaac 1189
Db 1097 gtgtaattcttaagattctgcaattcttaaacagcaatggtttagcagcttgcaata 1156
Qy 1190 gtttacaaggttaaattttagagtggtggaaaaagcaaatgycggtcgaacatctttgata 1249
Db 1157 aaattctaaacaataatgttgaatggtggaaaaaataaataacgcgtgaagacttactgaaa 1216
Qy 1250 aagcctatgattctcgatagctgctattatagtaataacttaaattttctgctagc 1309
Db 1217 atggtttagcgtatgcccgttactcttgcgaaatttacaagataataatgaatcttactgaact 1276
Qy 1310 taataaagaagttygaagcgtgaacgtgttlattgcaatcacccaaacagcttggatata 1369
Db 1277 taacaagaaggttacagcgagaacgtgttoatcgtattactacagcagaatggtgataaca 1336
Qy 1370 atattgtgtggttagcgcgttatccaatgttggtggaacgcatgaagcgtgaagcgt 1429
Db 1337 acattgtgtattttagctggtatttagccgtttaggttaaaagtccttagtggtaagcct 1396
Qy 1430 atgcagatgcttttgaagatgagcaagaagttagaagctgttccaatatattcttgatg 1489
Db 1397 atgtgatacgctttagaagaagcaaacacataaagccgaataattagtaacgttgat 1456
Qy 1490 cttaaaccttgatcatagacattagtaattcaaatggaatgggaaaaaagcgaacgcttgat 1549
Db 1457 cggcaaacggttatattgtatgtagtaattccggtgaagaaggaacacatcatctctat 1516
Qy 1550 tcaactcgccttgtttaacagcaggaactgaatcgaatggaacgtttaactaatgttaaat 1609
Db 1517 tcaagaacgcattattagcgcgggaacagagatacgttgaaacgcttaacaacaggttaaat 1576
Qy 1610 accttatattaaatgaatttgaatttcgaggtgttaaaaacttcggcaagttacaggtgag 1669
Db 1577 atgaatatattccaacatcaatataaaccgtgttagtagtgggaataattacagatggtg 1636
Qy 1670 aggcctatcttaaatattgatttctctlaaagtltatcagcgtgtgtagccgagacagagga 1729
Db 1637 cagcaagttcttaacttattgtaactaaagctgttgcaagctgtatgtgattgattagaca 1696
Qy 1730 cagaagagattggtctataatgttaatgcaaaa-----gctgcga 1768
Db 1697 atgctggaatgttaacttaaaacaaaagaaaataattatgccaacttggtgaaagt 1756
Qy 1769 atgacgatctcttgtgtgcagaaggttaaatatgatatgtgtgtagatgtagcacagatc 1828
Db 1757 atgacaacgcatattgtgtgtctggttcgtgacgcggaatgtatggtcgtgtaaggttacgac 1816
Qy 1829 ggtctctctatagtaaaagcagagatttggttaatatattcagtagatgtagtcaggtgcaa 1888
Db 1817 gagtctcactag---ccggtgaacatcatgtgtttaaactatgtgtaaccaaaagaga 1873
Qy 1889 cagaagaagcagttataacagttatcogtaagttgttcgtaggtgatacttaccagaag 1948
Db 1874 ccgaagcaagtagtataaccgtaaatcgttctgttagaaaccggtlaaagcactaacagaa 1933
Qy 1949 ttgtgaagcgtlcaagaacaaagttggtgtaacgtatgtaacatcactcaatctgatt 2008
Db 1934 tgacttcaaccataccacacgttagtggcacaacgtgtagaagaaaataagataatcgtcata 1993
Qy 2009 atgaattagaanaagttggtgtagtatacagttacccaataattgnaactcagtagaag 2068
Db 1994 gcaataacccagccacatg---ccggttattaccccaagaatcacttgaagcgttgaag 2050
Qy 2069 aagtaattggtttccaatttaagatgatacttaagaagttcaattcaacagacatatcc 2128
Db 2051 aaattactcgttatacacaatacagatctcttcaaggtlaagttcaatgaatgcttca 2110
Qy 2129 ataggtgtgaagtgatgaattactcogattggtgtgtgtgtagcagccgttcttggt 2188
Db 2111 acggtgtgtgtgtgtcgtataactatgacggtgaacgagcaatgacgcttatttggt 2170
Qy 2189 gtaaaagcaacgatacgaacttctcgtgagatgaagcgatgatacttaactcagatgcgttctg 2248
Db 2171 gtaaaagcgatgatattctcgtatcgtgtgaaatgtgtatgttacttaactcagtcggtgaag 2230
Qy 2249 gtgatagtatttaaaatggtggtgtgtgtatgtatgtctatcttccgtgaagaggtatg 2308
Db 2231 gcaacgacctattacaacgtggtgcaaggtcgatgatatcttcgttcaacgttaaaagcgatg 2290
Qy 2309 gtaatgatacttgtacatgycgacgycgaatgataaataatagcatgtgcagatgcaata 2368
Db 2291 gtaatgatatattacgcgattcgtacgagcaatgataaataatatactctcgtattggaact 2350
Qy 2369 tatctgatatatgatgtgaacgttaacaaagaggtatataagttaaacgaatgatact 2428
Db 2351 taanaaggtttaaactattgaaaagtttaaaaa---taactctgtcatcacgaattagaanaa 2407
Qy 2429 caggttagtattacaatccaagatggttaacatacaatattcaaaaa-----tt 2479
Db 2408 aagagaaggtgacacattcaaaacgtgttcggaaggtgtattgttgcgaagaagtgccta 2467
Qy 2480 atcaagtaataaacaagcatcaaaaattgaacaaacttggatlaaagatggttata 2539
Db 2468 attataaagcaactaaagatgagaataatcgagaataatcactcgttcaaaaatggtgcgagga 2527

QY 2540 tcacttcgcatcaaatgataaattt 2567
Db 2528 tcactcaagaagttgatcttat 2555

RESULT 3

AAT60032
ID AAT60032 standard: DNA: 3311 BP.

AC AAT60032;

DT 12-MAY-1997 (first entry)

XX Chimeric protein #1 coding sequence.

XX RTX cytotoxin; cytokine; immunogen; chimeric protein; cytokine; vaccine;
KM Interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; pneumonia;
KM Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;
KM fibrinous pneumonia; cattle; therapy; ds.

XX Synthetic.

Key Location/Qualifiers
CDS 1..3297
FT /*tag= a
FT /product= chimeric protein #1

US5594107-A.

14-JAN-1997.

22-AUG-1990; 90US-0571301.

20-DEC-1993; 93US-0170126.

22-AUG-1990; 90US-0571301.

16-OCT-1991; 91US-0777715.

(CIBA) CIBA GEIGY CANADA LTD.

(UYSA-) UNIV SASKATCHEWAN.

WPI: 1997-099529/09.

P-PSDB: AAM13866.

Immunogenic chimeric proteins comprising cytokine linked to RTX
toxin - useful in vaccines, esp. against shipping fever in cattle
Claim 10; Column 25-32; 56pp; English.

AAT60032 and AAT60033 represent the coding sequences for immunogenic
chimeric proteins of the invention. This sequence represents a chimeric
protein containing the bovine interleukin-2 (IL-2) sequence and a
leukotoxin sequence. The chimeric proteins of the invention comprise a
cytokine, selected from interleukin-2 (IL-2) and gamma interferon (gamma
IFN), linked to at least one RTX toxin epitope (preferably the sequence
shown in AAM13865). The RTX toxin used to provide the epitope sequence
is preferably a leukotoxin, especially the full-length Pasteurella
haemolytica leukotoxin. Alternatively, the leukotoxin is a truncated
leukotoxin lacking leukotoxic activity, especially LKT352. The chimeric
proteins can be used for the production of vaccines against respiratory
diseases such as pneumonia, particularly fibrinous pneumonia caused by
P. haemolytica, including shipping fever in cattle.

Sequence 3311 BP; 1113 A; 592 C; 699 G; 907 T; 0 other;

Query Match 29.3%; Score 815.6; DB 18; Length 3311;
Best Local Similarity 60.1%; Pred. No. 1e-170;
Matches 1344; Conservative 0; Mismatches 964; Indels 60; Gaps 9;

QY 39 aggtgtgaattcaacaagctcgattaaataattacttgctatcccaagat-- 96

Db 531 agcgcgagcttctttaaataactgaggcaaaaaataatcctctatattcccaaat 590
QY 97 ----tatgctcgcaaaaagctgggactttaattttaaagctgctgataat 152
Db 591 ccaatatgatactgacaagaagtaatgctttacagatttagtcaagcgcgcaagat 650
QY 153 aggtattgctgtttagcgaagaagccttaacacatgaaacgaanaaatctgtga 212
Db 651 ggggattgaggtacaaagaagaagcgaataatattgcaacagcccaacagtttag 710
QY 213 caagtaaaactgactctctcctcacaacactggtatgctattctgcgaacaaat 272
Db 711 cagatcaaacgcgctattgcttaactgagcggtgctattgctatccgcctcaaat 770
QY 273 agaaaagcttcaaaaaaacattctaccaaagtagcgaaggttagacagtgtaga 332
Db 771 tgataaattgctacgaaa-----actaaagagcgcaagcattagttctgcga 821
QY 333 aaatattgctgtaaatggttaagaagtaatgatatatacaacttaagctctttt 392
Db 822 aagcatctgacaataatgcaataaagccaacgtaattatctgcacccaactatct 881
QY 393 gggcactgcatlagcggtatagaacttgattctttaaacaanaagctgctgacc 452
Db 882 aggtcagatattgctcgatgagatttagatgagccttaacga---taacagcaaca 938
QY 453 tgatgcttgctaaagctagattgacttgattaaatgataatgtgaatctatca 512
Db 939 acatgctcttgctaaagctgcttgagtaacaaatcattatgataaattatgttaa 998
QY 513 gagtactcaaaagcattgttcacacaggttagcaaggttaggttctactatc 572
Db 999 ttcagtaaaaacactgacgaatttggtagcaaatatgacttctgttcaaaactaa 1058
QY 573 gcaagctaaaggctctcctaataatagaacaaagctgcaaaacttaaat---tttctaa 629
Db 1059 aatatcaaaagccttaggagcttaggagacaacccaataatcgtgagctgataa 1118
QY 630 aacaactctgtgttggaataatctctgttgcatacagcatcttcgacgcttgc 689
Db 1119 agctggccttggtttagatgtattctcagggcattatctggcgcaacgctgcat 1178
QY 690 tttagcgataaaaatgcatcgactcgacgcgcaaaaagctgctcgaggttgaatga 749
Db 1179 acttgagataaaaatgcttcaacacgctaaaagtggtgctggttgaattgcaaa 1238
QY 750 tcaagttattggttaatgtaacaaaagcaattcttcatagttttagacaacgtgtgc 809
Db 1239 ccaagttgttgaatatataccaagaacgcttctctctcaatttagccaacgtgtgc 1298
QY 810 tgctgctatacaactactggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgc 869
Db 1299 agcagattattcttcaacggtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgc 1358
QY 870 aattagcttcttgacattatgaatgacgaagaataatcaacatgacgaatgcttga 929
Db 1359 gatagcccatgacatctggtcggtatgtcggttaatttaacacagcaaaaagttaga 1418
QY 930 tgaatttgcgaacaaatctgcgaataatttgcgtatgttggtggtggttgcgtgata 989
Db 1419 gagttagcgcaagcgtttaaaaaattagcatgacggtgagataattattagcagata 1478
QY 990 tcaagctgc 1049
Db 1479 tcaagcggtggtgc 1538
QY 1050 agttctgctgc 1109
Db 1539 tatgtctgc 1598
QY 1110 attagttgaggtgc 1169

Db	1599	atcagatctcgggattaccoggtgtaattcttcacggtcttcgcaattcttcaaacagcaat	1658
Qy	1170	gtctgaaagctgtgcttaaccggtttacaagtgtaaaatttttagagctgggaaagcaaatg	1229
Db	1659	gtttgagcaagcttgcaaaataaatctcatacaaaaatttgatgattgggaataaaataca	1718
Qy	1230	cggtaagaactctttgttaaaagcgtatgattctcgttatgctgtttatgttaagctaa	1289
Db	1719	cggtaagaactctttgaaatcgtgtacagtgcccggtatctctggaatttcaagata	1778
Qy	1290	cttaaaattttgtctgagctaaataaagcttggaaagctggaacgtgtatgtgcaatcac	1349
Db	1779	tatgaaattcttaacgaacttaacaagaagttacagggaaagctgtcatcgtattac	1838
Qy	1350	ccaacaacgcttgaggataataatctgtgtgagttagcaggtattaccaattgggtgaag	1409
Db	1839	tcagcaacatctgggataaacaacattgtgtatttaagctgtgtatgaacgttttaga	1898
Qy	1410	catlaagacggaaaagctatgcacatgctctttgagaatggcaagaagctggaagctg	1469
Db	1899	agctcttagtggtaagcctatgtgtgacgtgttggaaggaagcaacaacataaagcga	1958
Qy	1470	ttccaatctactttgagatgctcaaaactggtatcabaagacatgataatccaatgggaa	1529
Db	1959	taatttagtacaagttgattctcgcaaacggtattatttgaatgtgagtaactcggtaaac	2018
Qy	1530	aaaaacgcaagcgttgcatcttcaacttcgcttggtaacagaaggaactgatacgtga	1589
Db	2019	gaaaaactcgacataltcttacaagaagccatattgacgcgggaagacagacatcgtga	2078
Qy	1590	acgttaactaaatggtgaataactcctataatlaagctttaaactltagcagctgtaaa	1649
Db	2079	acgcgtacaacaacggtgaataatgataatattacccaagccaatattacacggttagag	2138
Qy	1650	ctggcaagttacaagatvgagagagcctagttctaataatgattctctcaagttatlaag	1709
Db	2139	ctggaaaacttaacagatggtgcaacaagttctaccttgatttaacacgtgtgtcaag	2198
Qy	1710	tgtgacgcgagacgaagagcgacaacagagatttgtctcaatagtglaatgcaaaa-----	1761
Db	2199	tattgttatgatttagttagacatgcttggaatgtgaactaaaccaaagaacaaaattat	2258
Qy	1762	-----gctggcaatgacgatacttgtgtgtgccaaggtgaataatgtaattga	1808
Db	2259	tgccaactgtggaaggtgtgatacacaagattgtgtgtctgtgaacgcggaaattga	2318
Qy	1809	tgtgtgagatgtagacagatcgtctctctctatagtaaaagcggagatttgtaatat	1868
Db	2319	tggcgtgtggaaggttagacgcaggttcaactag---ccgvggaactaagtgctttaac	2375
Qy	1869	tgtagatgtagagatgcaacagaagcaggcaggtatacagttacatcgttaagtgctg	1928
Db	2376	tattgatgcaacaaagacggagcaaggtagtataccgtaaatcgttctgtgagaac	2435
Qy	1929	aggtgatatactacatgaagtgtggaagcgttcaagaacaaagctgggtgaacgtactga	1988
Db	2436	cggtaaaagcactacaagaagtgacttcaaccataccgcaattggtggcaacogtgaaga	2495
Qy	1989	aactatccagtatcgttatgatgatgaataaagaaagttgggtatgtatcatcagttacga	2048
Db	2496	aaaaatagataltcgtcatagcaataacacgacacatg---ccggtattacccaaga	2552
Qy	2049	taatttgaatatcagtaagaagaatgtgttcttcaaatttaatgatgtattcaaaagttc	2108
Db	2553	taccttgaagcgtgtgaagaaattacggtatacacaatacgaatcctttaaaggtag	2612
Qy	2109	taaatcaacagacatcttccatgggtggaagagatgatttactcatggtggtgtgtg	2168
Db	2613	taagttcaatgatgctcttaacaggtgtgtgtaggtgtgatatactattgaaggtlaagcag	2672
Qy	2169	tgcagacgcgtgtgtgtgtgtaaaagcaacgatacgaacttctggaagatgaagcgtga	2228
Db	2673	caatgcagcctattctgtgtgtaaaagcgatgataattctcgaatgtggaatgtgtatga	2732

QY	2229	tttaactgatggcggttcctggtgatagtatataatgggtgtgtcgtgtaagtatctcta	2288
Db	2733	tttatacgaatggcggttaagaagcaacgacctattacaacggttgcgaaggcgatgatattt	2792
QY	2289	tatcttcggaaaggtgatgtatgaatgatacttgttaacgttgacgacggaatgataatc	2348
Db	2793	cgttcacgcgtaagaagcgatgtgaatgatattattacacgattcttcgaaggcaatgataatc	2852
QY	2349	agcatttgcagatgacaatatatctgatatattatgatattgaacgttaccagaagaaggtattat	2408
Db	2853	atcatctctgtatctcgaaacttaaaagaatttaacatttgaaaaaaglttaaca---taactc	2909
QY	2409	agttaaacgaatatcatctcaagttcagttatlaacatacacaagaatggtatcatacatacaaa	2468
Db	2910	tgtcatccagcatgacaaaagaagaagaaggtaccattccaacactggttcgcgaagctga	2969
QY	2469	tttacaaca-----ttatcaagaatataaacaagatcatataatttgagcaactat	2519
Db	2970	ttttcttaagaagaatgacctatttttaagaacaataagaatgagaanaaatctgaagaacatcat	3029
QY	2520	tggtaagaatgtagttatatacatcacttcgcgtcaaatgtataaatttt	2567
Db	3030	cggtcaacaatggcgagcggaatcacctaacaagaatgtgatcatcttat	3077
RESULT 4			
AAAT2483			
ID	AAAT2483 standard; DNA; 311 BP.		
XX			
AC	AAAT2483;		
XX			
DT	19-DEC-2000 (first entry)		
XX			
DE	Bovine IL-2/Pasteurella haemolytica leukotoxin fusion gene.		
XX			
KW	Bovine IL-2; interleukin-2; leukotoxin; LKT; respiratory disease;		
KW	pneumonia; shipping fever; cattle; livestock; anti-Pasteurella vaccine		
KW	immunogen; ds.		
XX			
OS	Chimeric - Bos taurus.		
OS	Chimeric - Pasteurella haemolytica.		
XX			
FH	Key		
FT	CDS		
FT	Location/Qualifiers		
FT	1..3297		
FT	/tag=a		
FT	/product="Bovine IL-2/Pasteurella haemolytica		
FT	leukotoxin fusion protein"		
PN	US6096320-A.		
XX			
PD	01-AUG-2000.		
XX			
PF	20-OCT-1997; 97US-0954418.		
XX			
PR	20-DEC-1993; 93US-0170126.		
PR	22-JUL-1996; 96US-0681479.		
PR	22-AUG-1990; 90US-0571301.		
PR	16-OCT-1991; 91US-0777715.		
XX			
PA	(UYSA-) UNIV SASKATCHEWAN.		
PA	(CIBA) CIBA GEIGY CANADA LTD.		
XX			
PI	Campos M, Hughes HPA, Potter A;		
XX			
DR	WPI; 2000-531543/48.		
DR	P-PsDB; AAB21073.		
XX			
PT	Vaccine for stimulating immunity against pneumonia comprises chimeric		
PT	protein comprising gamma-interferon and leukotoxin derived from		
PT	Pasteurella haemolytica		
XX			
PS	Example 1; Column 25-32; 56pp; English.		

xx The invention relates to a novel vaccine composition comprising an
CC immunogenic chimeric protein that comprises gamma-interferon (gamma-IFN)
CC or an active fragment thereof, linked to an epitope of a Pasteurella
CC haemolytica leukotoxin (LKT). Pasteurella species, especially Pasteurella
CC haemolytica, are responsible for respiratory diseases in a range of
CC agricultural animals, most particularly cattle, but also sheep, pigs,
CC horses and fowl. Shipping fever is the most economically important
CC respiratory disease associated with Pasteurella species, affecting
CC 15-30% of exposed cattle and resulting in a 2-5% mortality rate in the
CC exposed population. The vaccine composition of the invention is
CC is useful for preventing or ameliorating respiratory diseases such as
CC pneumonia, particularly shipping fever pneumonia, in livestock. The
CC present sequence represents DNA encoding a fusion protein comprising
CC bovine Interleukin-2 (IL-2) and Pasteurella haemolytica leukotoxin.
CC which may also be used as an anti-Pasteurella vaccine.
xx
SQ Sequence 3311 BP: 1113 A; 592 C; 699 G; 907 T; 0 other;

Query Match 29.3% Score 815.6; DB 21; Length 3311;
Best Local Similarity 60.1% Pred. NO. 1e-170;
Matches 1544; Conservative 0; Mismatches 964; Indels 60; Gaps 9;

QY 39 aggcctgattcacaagaagctctggtataaaaaattcttactggtctcccaagaat-- 96
DB 531 agcggcgacgtctcttaaaaaactggggcaaaaaaatctctctatctcccaaatla 590
QY 97 ----tatgacgcgaanaaaggctggaactttaatgtattttaaagctgtgtaaat 152
DB 591 ccaatatgactgacaagaagtaatggtttacagatttagccaagcgcggaagatt 650
QY 153 aggtatgctcgttttagagaagaagcctaaccctgaacacgcaaaaaaatcgttga 212
DB 651 ggggattgaggtacaaaagaagaacgcaataatctgcaacgctcaacgaatttgg 710
QY 213 cagcgaatacagttctctctctccacaacactggtatctctatcttcgcaaaaatt 272
DB 711 cagatccaacacgcgtatggtcttaactgagcggtggtatggtatctgcgcccaat 770
QY 273 agaaaagttcttcaaaaaacatcttacaataagtttagcgaaggttagacagttgta 332
DB 771 tgataaatgtctacagaaa-----actaaagcagcgcaagattagtttcgcgca 821
QY 333 aaatattgattcgttaaataggtaaaagcaagtaattatctcaacaataagctctttt 392
DB 822 aagcattgtcaaaaatgcaaaaataaagccaaactgtatctatctggtcattcaatcttt 881
QY 393 gggcactgactagcgggtatagaactgtattcttaacaaaaggltgactgcacac 452
DB 882 aggtcgaattctgctcggaatggatttagatgagcgcttacaaga---taacagaacca 938
QY 453 tgatgctttgcttaaaagtagtatgactgtatgataatagataatgtaactctaca 512
DB 939 acatgctctgcttaaaagctgctgagactaacaatctcatatgtaaatatgtaacta 998
QY 513 gagtactcaaacgattggaactttcttcacagtttagcaaaagttagttctactata 572
DB 999 ttccgttaaaaacactgtgcgaattctggtgagcaaatlttagcaatttggttcaaaactaca 1058
QY 573 gcaagcgtaaagctctctctataatagaagaagaagttgcaaaaacttaaat---tttctcaa 629
DB 1059 aaatatacaaaagcttaggacttaggagacaacatacaaaaatatacgtgactgtgtaa 1118
QY 630 aacaatcttggtttggaataaatactactggtttgctatcagaagcttctcagaagcttcg 689
DB 1119 agcttgaccttggttagatgtatctcagggctatctacggcggaacagctgactgt 1178
QY 690 tttagcgataaaaatgcatcgactgccaanaaagttgctcgaagttttgaatgaacaa 749
DB 1179 acttgcaataaaaatgcttcaacagctcaaaaagttgggtgcggttttgaatttgccaaa 1238
QY 750 tcaagttatgtgtaatgtaacaaaagcaattctctcatatgttttagacaacagtggtgc 809

DB 1239 ccaagttgtgtaatataccaaaagccggttctctcttaccatttagcccaagcgtgtgc 1298
QY 810 tctgtctataactactggtgtcgtgtgcttcaattactatcatcgatatactgtgc 869
DB 1299 agcagttattcttcaacatgagccgtgtgctgttcaattgcttactggtctcttcgc 1358
QY 870 aattgctcttgcattatgaaatgacgagataaattcaatctcgtcaatgctctga 929
DB 1359 gattggccatgaagacttgcgcggtatgcgataaattcaatcagcaaaagtttga 1418
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QY 1050 agttctgctggtgttccgcgtcgtgtgtagatcgtcgtgtgtgtgacacgattgcact 1109
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DB 1779 tatgaaattcttaccgaacttaacaagaaggttacaagcagcgtgtcatctatctac 1838
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QY 1410 catgaagcggaaaagcgtttagcagatgtctttagaagtagtgcgaagaagttggaagctg 1469
DB 1899 agtctttagtgaagcgtttagtgaagcgtttagaagtagtgcgaagaacacattaaagcga 1958
QY 1470 ttccaattacttggatggttaaacgtgtatctcaatagacattgaattcaaatgysaa 1529
DB 1959 taatttagtacaagttggtatcgcgaacgggtattttagatgtggaataattcgggtaagc 2018
QY 1530 aaaaacgcaagcgtgtgcatlctactcgccttgtttaaagcaggaactgaatcagctga 1589
DB 2019 gaaaactcagcatatctatttaccagaagcattatttgcgcgggaacagagacatctga 2078
QY 1590 acgtttaactaatgttaataactctctatattataatgaatgaatcgcgaagcgtgtaaaa 1649
DB 2079 acgcgtlaacaagaagtaataatgaaatatacttcaagcgtcaatlaaacggttagatag 2138
QY 1650 ctgcaagtttacaatgtagagagcgttcaaatctgaatttagatctcctaagttcagag 1709
DB 2139 ctggaataattacaagatgtgtgcagcaagttctacactttagattcaactaaagttgttcagcg 2198
QY 1710 tglagccagacagaagcacagacagatgtgtctaatagtaaatgtcaaaa----- 1761
DB 2199 tatgtgatgtgattagcaaatgtcgaatgttaactaaacaaagaacaaataat 2258
QY 1762 -----gcttgcaatgacgatatcttctgttgcgaaggttaaatgaatgaatga 1808
DB 2259 tgcgaacttgggtgaaggtgtagacaacgtatcttctgttctgttgcagcaggaattga 2318
QY 1809 tgggtgagatgtagacacggtcgtctctctatagtaagaacggaagatttggtaatttcc 1868

OY	467	aagctagatattgacttgatataatgagataattggtataatctatctcaagctactcaaacga	526
Db	437	aagctctgttgaggctctaacaaattctatcatatggaataattctgaattcagtaaaacac	496
OY	527	ttgagaactttcttccacagtttagcaagtttggtttctctatctatccgaagctaaagct	586
Db	497	ctgcagatctnctgagcaaatctagtaaatcttggtctcaaaaactaaaaataatcaagct	556
OY	587	ctctcaataatagaaaagaattgcaaaacttaaat---ttctctcaaaaactcttggt	643
Db	557	taggagctcttagagagacaaactcaaaaataatcgtgtagcttgatataagctggtcttgct	616
OY	644	tggagaataatctactggttctgctatccagcaattctgcaggtcttgctttagcggataaa	703
Db	617	tagatgttatctctcagggctctatctcggcgcaacagctgacttactctgtagataaaa	676
OY	704	atgcatactgactgcgcaaaaaggtctgcgcaggttttgaattaaagcaatcaagtttgta	763
Db	677	atgcttctcaacagcctaaaaaagctgggctggcgggttttgaatttgcgcaaaccaagtttgta	736
OY	764	atgcacaacaaagcaattctctctcatagttttagcaacaagtttctgctgctcatcaa	823
Db	737	atatattcaaaagcggttctctctcttaaatctttagccaaagctgtgcagcaggttatctt	796
OY	824	ctactgctgcbtctgctgcgttcaatactcatcagatagtgttgcaattagtcctcttg	883
Db	797	caactggcgctgtgcgtctgacttaattgctctctactagttctctcttgagttaccatag	856
OY	884	catttatgaaatgcagcagataaattccaatccatgcaatgctcttgatgagtttgcaaac	943
Db	857	catltgcggatctatgcgataaatttaatactgacaanaagttttagagagtatgcgcgac	916
OY	944	aattcggaaatttggctatgagtgagggaatcatatttggctgtaatactacgctgttg	1003
Db	917	gctttaaaaaatctaggtcatagcagcgagataatttatctagcagaatacatcagcgggaacag	976
OY	1004	gtaactatggaagcttcaattcaactacatatttagtcagcattagtgccagtttctctgttg	1063
Db	977	ggaactatgatgcaatcggttactgcgaataataacgcgacttgcgctatctgctgttg	1036
OY	1064	tttcgcgtcgtcgtctgtagatctgcgtgtgttgacgcgactgacatattagtctgagtg	1123
Db	1037	tgctcgtcgtgcagccgcgctcgttatgtgtcttccacggattcctctatctagatctggga	1096
OY	1124	ttcaaggaattgatctctcgggaattttagaagcgttctaaagaagcaattgtttgaagtgctg	1183
Db	1097	ttaccggctgtaattctctcaagatctctgcgaatatcttaaaagaagcaattgttgagcagtg	1156
OY	1184	ctaacgcgtttacaaggtgaanaattcttagatctgtagaagaaagcaaatgctcagaaactt	1243
Db	1157	caaatataaattctataaacaataatctgttagaatgtagaanaataataatcaggtlaagaactact	1216
OY	1244	ttgataaaggctatgatactcgtttagtctgattatcttagcttaataacttaaattttgct	1303
Db	1217	ttgaaaaatgggttccagatgcgcgtctatctctgcgaaatttcaagaatataatgtaatctctac	1276
OY	1304	ctgtagcctaaataaagggttggaaagctgcgaacgcgttatattgcaatcccaacaagcttg	1363
Db	1277	tgaacttaaaccaagaagtcttacaagcgagaagcgtgtccatccctatcttaccagccaatggg	1336
OY	1364	ataataatattggttgagtttagcagcagatctataccaatcttggttgaaacgctaataagcggaa	1423
Db	1337	atacaaacatcttgatatttagctgcgttatcttagccggttttagtgtaaaaagctcttggtgta	1396
OY	1424	aagctatctgagatgcttttggaaatgtagcaagagaagattggaagctggttccaatattact	1483
Db	1397	aagcgtatctgtagatcggtttggaaggaagcacaacacattaaagcgcgataaatattgatacgt	1456
OY	1484	tgggttgtaaaacgcgtgatcatatgacattgaatttcaaatatgtaggaaaaaagcaagcgtc	1543
Db	1457	tgggtcttcggcaaacggaattatctgtagttagtgaattcgtgttaaagcgtgaataaccagcata	1516
OY	1544	tgcattctacactgcgctttgtttaaagcagcgagacgttaatccaagttgaaagctttaactatg	1603

Db	1517	tcctatttcagaaacgcccattctttagccgcgggaacagagcatgcytgaacgcgttaacaaacag	1576
Qy	1604	gtaaatactcttaattatnaagtttinaaatttcgagacgtttinaaagacgggaatttcag	1663
Db	1577	gtaatatgatataataataccaagctccaaatlaaacccgttgatagtcgcygnaaatlaag	1636
Qy	1664	atvgagagvgctagttctcaaatctgagatcttcctinaaagttlaatacgtgtgaacgagacag	1723
Db	1637	atggttcagcaaggtctcaactcttgatttacttaacagctgtgtcagcgatattggtatctgaat	1696
Qy	1724	aagcgacagacgagatctgtctcaatctgtaaatgycaaaa-----g	1762
Db	1697	tagacaatgcytgcgaatactgtaacaaaccaaagaacaaataattctgcacaactgtgt	1756
Qy	1763	ctgcgaatcagagatattcttgtgtgtcgaaggtgaataatgtgatatctggtgtggagatggac	1822
Db	1757	aagvgagagaaacagctatctgtgtgtctgtcgtgtgaacgaggaatactgaaatgagcgtaaggt	1816
Qy	1823	acgaatcgtctctctcaatagtaaaacagagagatttvgtaatacttactgttaagtgcga	1882
Db	1817	acgagacgagttccactatag---ccgtggaacactatggtgtctttaaactttgatacgaaca	1873
Qy	1883	gtgcacaacagacgagcagttatacagtttaacgttaacgttgcgtccaggtgatatctaac	1942
Db	1874	aagagacagcagcaaggtagttatacgttaaatcgtgtctgtaagaaacggtataaacactaac	1933
Qy	1943	atgagatgtgtgaagcgtcgaagaacaaaggtggtgaatacgtctcaactctccaggtatc	2002
Db	1934	acgagatgtacttcaaacccataacgcgtatcgtgtgcgaacccgttgaaagaaataatgatatcc	1993
Qy	2003	gtgattatgtaattagaanaagcttgggttagtgttatacgtctacccagataatttggaaatcacg	2062
Db	1994	gtcatagcaataaacacagccacatgt-----ccggttatatacccaagaatataccttgaagctgt	2050
Qy	2063	tagaagaagtaattgtgtcttcaattttaaagtatgatactgatacgaaggtctaaattcaacgca	2122
Db	2051	cttgaagaataattatcgtatacatccataacagatatcctttaaggtagtagtaatttcaatgtgt	2110
Qy	2123	tattccatagtggtgtgaaaggtgatacttactcgtatggtgtgtgtgtgtgtgaacccgctgtc	2182
Db	2111	cccttaaacgtgtgtgtatcttaccgtatactatgatactgatacgtatacgtgcgaatgacgcttat	2170
Qy	2183	cttgggtgaaaggtgaacagatcgcagctcttcctggagatgaaggtgatacttactcgtatgcg	2242
Db	2171	cttgggtgttaaggtgcgatacttccgtatcgtgtggaatggtgtatcttactcgtatgcg	2230
Qy	2243	gtctccgtgtgactgatactttaaactgt	2302
Db	2231	gttaaggtgaacgactatttaccgtgtgtgcgaaggtgcgatacttctgttcacgttaag	2280
Qy	2303	gtgatgtatgatacttctgtacgatggtgcgcggtgcaatgataatctgacatttgcagatgt	2352
Db	2291	gcgattgttaaggtatatacttaccgacttgcgtgcgcaatgataatcttactcctctgtat	2350
Qy	2363	caaatatactcgataattatgtatgtgaacgtgcacaaagaggtatattatgtttaaacgaaggt	2422
Db	2351	cgaactctaaagatttacaacttggaaaagttaaaaa-----taactctgtcatcagtaata	2407
Qy	2423	atcatctcgtatgattatnaataccaagatgtgatactaaatcaaatcttaacaaa-----	2477
Db	2408	gcataaaagaggaaggtgacatctcaaaactgtgtccgagaggtctgtatttgcctaagag	2467
Qy	2478	-----ttatcaaggtatataaaacagatcatataaatctgagcaactaattctgttaagatgtga	2533
Db	2468	tgctaatattataaagcaactaaagatgagataaaatcgaagaaatcatcgtgtcaaaatgtgcg	2527
Qy	2534	gtatacatccttcgcatcaaatgtgaataaatctt	2567
Db	2528	agcgatcatccctcaaaagcaagttgatacttat	2561

ID	AAQ41323	standard; DNA; 2861 BP.
XX	AAQ41323	
AC	AAQ41323;	
DT	23-AUG-1993	(first entry)
XX		
DE	Rotavirus VP4-leukotoxin gene fusion.	
XX		
KW	Vector: LKT 352; flanking; recombinant; antigen; somatostatin;	
KW	gonadotropin releasing hormone; rotavirus viral protein 4; ds;	
KW	carrier protein; lactation; reproduction; SRIF.	
XX		
OS	Synthetic.	
XX		
PH	Key	Location/Qualifiers
FT	misc_feature	1..2778
FT		/*tag= a
FT		/note= "recombinant leukotoxin "
FT	misc_feature	2779..2861
FT		/*tag= b
FT		/note= "Rotavirus VP4 DNA"
PN	W09308290-A.	
XX		
PD	29-APR-1993.	
XX		
PF	15-OCT-1992;	92WO-CA00449.
XX		
PR	16-OCT-1991;	91US-0779171.
PR	14-OCT-1992;	92US-0960932.
XX		
PA	(UWSA-) UNIV SASKATCHEWAN.	
XX		
PI	Hughes HPA, Potter AA, Redmond MJ;	
XX		
DR	WPI: 1993-152482/18.	
DR	P-PSDB; AAR34548.	
XX		
PT	Immunological carrier system with enhanced immunogenicity -	
PT	comprises chimeric protein comprising leuco:toxin peptide or	
PT	homologous protein fused to antigen esp. somatostatin or	
PT	gonadotropin releasing hormone	
XX		
PS	Example 2; Fig 10; 95pp; English.	
XX		
CC	Oligonucleotides contg. sequences from bovine Rotavirus viral	
CC	protein 4 (VP4) gene were constructed on a Pharmacia Gene	
CC	Assembler using standard phosphoramidite chemistry. The oligo-	
CC	nucleotides were annealed and ligated into vector pAA352 (contg.	
CC	the Pateurella hemolytica leuko-toxin gene) which had been digested	
CC	with BamHI. The ligated DNA was used to transform E. coli strain	
CC	MH3000. Transformants contg. the oligonucleotide inserts were	
CC	identified by restriction endonuclease mapping and the recombinant	
CC	plasmid designated pAA501. The chimeric protein produced from the	
CC	plasmid works to bring about a larger immune response than the antigen	
CC	alone, i.e. the leukotoxin works as a carrier protein.	
CC	See also AAQ41317-22.	
XX		
SO	Sequence 2861 BP; 947 A; 504 C; 615 G; 794 T; 1 other;	
XX		
QY	Query Match	29.3%; Score 815; DB 14; Length 2861;
	Best Local Similarity	60.2%; Pred. No. 1,3e-170;
DB	Matches 1538; Conservative	0; Mismatches 956; Indels 60; Gaps
XX		
QY	53 caaagctcgtatgaataaactcttacttgcgtatcccaagaat-----tatgatccgc	106
DB	29 caaaactcgtggcgcaaaaaaattatctctatattcccaaaattaccataatgatgac	88
XX		
QY	107 aaaaagctggagacttaaatgatattatataagctgcgtatgatagtgatgcgct	166
DB	89 aacaaggtatattgcttaccagattatgccaagcgcggaaggttgggattgaggtac	148

[illegible]

OY	1244	ttgataaagcgtatgatctctcgctatgcgcttattttagctataactataactaaattttgt	1303
Db	1217	ttgaaatattgtttagcagatgccggttatctctgtgcaatttcaagaataataatgatctttac	1276
OY	1304	ctggcgtcaataaagpatttggaagcgtgaacgcgtgtatctgcaatcccaacaacgttgg	1353
Db	1277	tgaacttcaacaagaagatttcaagcgcgaacgcgtgtcatctatctcagcagcaatggg	1336
OY	1364	ataataatattgctgagtttgcgcaggtatataccaatctgggttcaacgcataaagcggaa	1423
Db	1337	atacaagaatttggtgatttgctgcgtatcatccggttatccggtttagtgaaaaagtccttg	1336
OY	1424	aagcttatgcagatgctctttgaagatgycgaagaagattgaagcgtgttccataattact	1483
Db	1397	aagccttatgtagtcggtttggaagaagcaaacacattaaacgcatataatttagtcagt	1456
OY	1484	tgggtgtctaaacctcggtatcatatgacattgaattccaatgtyggnaaaaaacgcagcgt	1543
Db	1457	tggattctcgcaaaaaggtatatttgaatgtagatattcgggttaaaacgcgaatacagcata	1516
OY	1544	tgcattccacttcgctcttgtttaaagcgggaacgtgaatcagatgaaagctttaaataag	1603
Db	1517	tctattccagaagcgcatttttgaacgcgggaacagagcatcgtgaaacgcttacaacag	1576
OY	1604	gtaatactcttatattatataaatttlaaaattcggaaatgltlaaaaaactgcggaattacag	1663
Db	1577	gtaataatgatatattatataccaagctcaatatbaaacggtgtagatagcggaaattacag	1636
OY	1684	atggaagagcgtatgtcttaaatitgattctcttaagttatcaacggtgttagcggagacag	1733
Db	1637	atgggtcagacaaggtcttcaacttgcatttcaactagcgttgtcaagctatgtgattgaat	1696
OY	1724	aagccacaagcggagatgtggtcttaatagttaaatgtcaaaa-----g	1762
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OY	1763	ctggcaatgacgaatctcttctgttgcgtcacaaggtlaaaatgtatatgtatgtgtagatgac	1822
Db	1757	aagtgtagtgaacaagctattgtgtgtctcgtgatacgcggaatttgaatgtgcgtgaaagtt	1816
OY	1823	acgaatcggtctcttatagttaaagcggaggaattgtgtataattacgtgtagatgtgaca	1882
Db	1817	acgacgcagatgtcactataag---ccgtgtggaactatgtgtctttaaactatgtatcaacca	1873
OY	1883	gtgcaacaagcgaagcggaggttatcaaggtttaatcgtgaaggttgctcgaagtgatattcacc	1942
Db	1874	aagagaccgcggaaggaagtattatataccgttaaatccgttctgtaaaaaacggtataagcactac	1933
OY	1943	atgaagtttgtgaagcgtctcaagaagaaccaaaggtgtgtlaaaacgttctgaactaccagtatc	2002
Db	1934	acgaagtgacttcaaccataccgcatcttagtggcgaacgcgtgaagaaaaatagaatatc	1993
OY	2003	gtgatttatgaattaaagaanaagttgggtatgttatccagttctaccgataatttgaataccag	2052
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OY	2053	tagaagaagatgaatttggtcttcaatttgaatgagttatcaaaaggtcttaattcaacagcata	2122
Db	2051	cttgaagaataattcgtgtactcaccataacacgatatcctttaaaggtatgtatgttcaatgtag	2110
OY	2123	tattccatagtggtgaagcgtgaatcttactcagttgctgattgctgtgtgtygcagacgcgtgt	2182
Db	2111	cccttaacggtgtgtgtagcgtgtcgtatctatcttagacgtgaacgaacgtgaacgtccgttat	2170
OY	2183	ttgggtgttaaaagcgaacgatacgcattcttcggagatgaagcgaatgatacttactcgtatggc	2242
Db	2171	ttgggtgttaaaagcgtgaatctctcgaatgtgtggaataatgtatgtatttactcgtatggcg	2230
OY	2243	gtctcgtgtgaatgagttttaaagctggtgtgcgtgtaagatgtctcatatcttcttggaaag	2302
Db	2231	gttaaggtcaaacgaccttctacacggtggtgcgaaggtcgatatttctgtccacgttaag	2290
OY	2303	gtgattgtttaaagtaacttttagatgatygcacgggcgaatgatataatgaatttgcagagt	2362

Db	2291	gagatggtgaagatataattaccgattccgaagcgaatgataataattacattccttgat	2350
Qy	2353	caaatatcttgatatatgatgtgaacgtaccaaagaggtatagttaaacgaatg	2422
Db	2351	cgaaacttaaaagattttacatttgtaaagaattbaaca---taacttgcaccagaata	2407
Qy	2423	atcattcaggtagatttaacataccaaagaggtacataacatcaatltacaac----	2477
Db	2408	gcaaaaagagaagaatgaccatccaacgtgctccgagagctgatttgtgtaagaag	2467
Qy	2478	---ttatcaagaatcaaaaacgatatcatataattgagcaactattgtaagaagtga	2533
Db	2468	tgacctaatataaagcaactaaagaatgagaacacgaagaataatcagttcaaaatgcg	2527
Qy	2534	gtatatcatctccatccaattgataaaattt	2567
Db	2528	agcgatcacctcaagaacgattgtagtcttct	2561

RESULT 7

AAQ14238
ID AAQ14238 standard; DNA; 2794 BP

AC AAQ14238;

DT 15-JAN-1992 (first entry)

DE LKT352 gene.

KW Antigen; leukotoxin; vaccine; Ikta; ds.

OS *Pasteurella haemolytica*.

PN W09115237-A.

PD 17-OCT-1991.

PF 17-OCT-1991; 91WO-CA00170.

PR 05-APR-1990; 90US-0504850.

PA (UYSA-) UNIV SASKATCHEWAN.
XY

PI Acres SD, Barluk LA, Potter AA, Lawman MJP;

DR WPI; 1991-324967/44.
XX

PT Vaccines for Pasteurella haemolytica infection in cattle -
comprise sub-unit antigens from P haemolytica fimbriae protein

PT plasmin receptor, 50 K outer membrane protein and leukotoxin.

PS Disclosure; Fig 5; 92pp; English-
XX

The LKT352 gene was prepd. as follows: *lktA*, an *MaeI* fragment contg. the gene was ligated into the *SmaI* site of pUC13 to form pAA179. From this, two constructs were made in the p3ac-based vector, pDH432:*laci* digested with *SmaI*. One, pAA332, consisted of the 5' *AhaII* fragment from *lktA* while the other, pAA345, contained the entire *MaeI* fragment. Clone pAA342 expressed a truncated leikotoxin peptide at high levels while pAA345 expressed full length leikotoxin at very low levels. The 3' end of the *lktA* gene of pAA345 was therefore ligated to *StyI*/*BamHI* digested pAA342 to yield pAA352 contg. the LKT352 sequence. The protein expressed from the vector can be used to prepare a subunit vaccine with other *P. haemolytica* antigens, e.g. fimbrial protein, plasmid receptor or 50K outer membrane protein. The vaccines can be used to protect cattle from respiratory diseases such as pneumonia, esp. shipping fever pneumonia.

Sequence 2794 BP; 930 A; 487 C; 599 G; 778 T; 0 other;

Query Match 29.3%; Score 814.4; DB 12; Length 2794;
Best Local Similarity 60.2%; Pred. No. 1,8e-170;
Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

QY 53 caaagctgataaaaaattcttacttgctctcccaagat-----tatgaccgc 106
DB 29 caaaaactgggcaaaaaaatatctctctatctcccaaatatccaatattgatactg 88
QY 107 aaaaagctggactttaaatgatttataaagctgcgtatgaattagatgctgcgt 166
DB 89 aaaaagtaattggtttacggatttgatccaagcgcggaagaggttgggagttgaggtac 148
QY 167 tagcagaagagcctaatacactgtgaacagcaaaaaaatctgttgaacacagtaaatcagt 226
DB 149 aagaagagaagcgaataatattgtcaacagctcaaaccaagtttagacagatccaacg 208
QY 227 ttctctctcacacaaactggtatgtctattcttcgcaacaaattagaaaattcttcc 286
DB 209 ctattgcttaacttgccgtggtgcatctgttaccgcctccacaatattgataaatctgctac 268
QY 287 aaaaactctacaaatagttagccaaggttagacaggttagaanaaatattgatacgt 346
DB 269 agaaa-----actaaagcgcgcaagcattaggttctgcggaagcattgttaca 319
QY 347 aattagtaagaagaatgataatcatcaacatlaagctcttttgggcactgcatlag 406
DB 320 atgcaataaagccaacaaactgtatattctgcatctcaatctattttagcagatctg 379
QY 407 cgggtatagacttgattcttcttaatacaaaaagtgtgtgtgcacccgagcttggtc 466
DB 380 ctggaaatgatttagagtaggcttaccagaa---taacagcaacccaacagctctgtgta 436
QY 467 aagctatgactgacttgatataagataatgtgtaactcatctcagagtaactacaaga 526
DB 437 aagctgcttggtggtacacaatcttaattgaataatattgcttaattctgaataaacac 496
QY 527 ttgaagcatttctctacagttgcaaaagttaggttctactatactgcgaggtcaaaagct 586
DB 497 ttgacgaatttggtgagcaaatatagtaacttggttcaaaactcaaaaatacaaaagct 556
QY 587 tctctaataataggaacaagttgcaaaactaaat---tttctcaaaaacaaactgtgt 643
DB 557 taaggactttagaggaacaacccaataatcgtgtggaacttgataaagctgcgcttggtc 616
QY 644 tggaaataactactggttgcatacaggcatcttctgcaggtcttgcctttagcggataaa 703
DB 617 tagatgtatctcagggctattatcggcgcaacagctgcactgttactcttcgcagataaa 676
QY 704 atgcactgactgcaaaaaagttgctgcaggttttgataaagcaatcaagttatgta 763
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QY 1004 ttactatgaagctctacttaactaactatagtaacgcatataggtgcagttctgtg 1063
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DB 1037 tgcctgctgcacagcgcgctcggtattgtcttcacggatttcctattagatctcggga 1096
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DB 1097 ttacgggttaatttttaagattctgcgaattctcaaatcaagaacaaatgtttgcagcttg 1156
QY 1184 ctacccgtttacaaggtaaaattttagagttgggaaaaagcaaaaatgvcggtcagaactat 1243
DB 1157 caataaatactcaaaaacaaatgttagaattgggaaaaaataatcccgltlaagaaactact 1216
QY 1244 ttgataaagctatgttctcgtttagcgtctattttagcttaataacttaaaatttgtg 1303
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QY 1304 ctgagctaaataaagatttggaagcgtgaacgtgttatttgcaatcaccacaacagttgg 1363
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DB 1637 atggtgcagaagttcttactcattgatttaactaaagttgttcagcgtatgttgaat 1696
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DB 1697 tagcaaatgtctggaatgttaactlaaaaccaaagaaaataaattatgccaactgtgtg 1756
QY 1763 ctggcaatgacgatalcttgttgcgtgaaggtaaatgaaatattgtgtgagatggac 1822
DB 1757 aaggtgcagcaacgtaattgtgtgtctgtgtacagagaaattgtatvgcgtggaaggt 1816
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QY 2534 gtatataccttcgcgtcaaatgtataaatttt 2567
Db 2528 agcgtgatacctcaagaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2561

RESULT 9

AAQ44760
ID AAQ44760 standard; DNA: 2794 BP.

AAQ44760;

XX
XX
DT 06-Oct-1994 (first entry)

XX DE Recombinant leukotoxin from plasmid PAA352.
 XX XX Vaccine: outer membrane protein; OMP; Haemophilus somnus;
 KM Iron regulated protein; leukotoxin; Pasteurella haemolytica;
 KM LKT352; ds.
 XX OS Pasteurella haemolytica A1 (strain B122).
 XX XX
 FH Key
 FT misc-RNA
 FT 1..30
 FT Location/Qualifiers
 FT /tag= a
 FT /note= "vector sequence"
 FT 1..2781
 FT CDS
 FT /tag= b
 FT /label= recombinant_leukotoxin_peptide
 FT 2772..2794
 FT misc-RNA
 FT /tag= c
 FT /note= "vector sequence"
 FT CA2099707-A.
 XX PD 03-JAN-1994.
 XX PF 29-JUN-1993; 93CA-2099707.
 XX PR 02-JUL-1992; 92US-0908253.
 XX PA (UYSA-) UNIV SASKATCHEWAN.
 XX PI Harland RJ, Potter AA;
 XX DR WPI: 1994-092909/12.
 XX P-PSDB: AAR50291.
 XX PT Haemophilus somnus outer membrane protein extract -
 XX PT enriched with iron-regulated proteins, opt. contg.
 XX PT Leuco:toxin antigens, for use as vaccine
 XX PS Claim 5; Fig 5; 78pp; English.
 XX XX
 CC A vaccine comprising an outer membrane protein (OMP) extract of
 CC Haemophilus somnus enriched with iron regulated proteins is new.
 CC The vaccine pref. further comprises an immunogenic leukotoxin
 CC polypeptide, esp. an immunogenic pasteurella haemolytica leukotoxin
 CC homologous to LKT352. Example 1.2 describes the prodn. of
 CC P. haemolytica recombinant leukotoxin from PAA352.
 CC Two expression constructs were made. One, PAA342, contained the
 CC 5'-Ahal fragment of the ltkA gene, while the other, PAA345,
 CC contained the entire ltkA gene. PAA342 expressed a truncated
 CC leukotoxin peptide at high levels, while PAA345 expressed full
 CC length leukotoxin at very low levels. Therefore, the 3' end
 CC of the ltkA gene was ligated into PAA342, yielding plasmid PAA352.
 CC LKT352 or new leukotoxin is 98% homologous to authentic
 CC leukotoxin.
 XX CC
 XX Sequence 2794 BP; 930 A; 487 C; 599 G; 778 T; 0 other;
 SO
 Query Match 29.3%; Score 814.4; DB 15; Length 2794;
 Best Local Similarity 60.2%; Pred. No. 1.8e-170;
 Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

Db 149 aaagaagaagcgaataatgtgcaacgctcaaacagtttaggcagatccaacg 208
 Qy 227 ttcctctccacacaaacgtggtatgtcttctcgaacaaattgagaagtcttac 286
 Db 209 ctatgtgcttaactgagcgtgcatgtgttatccgcctccacaattgataatctgtac 268
 Qy 287 aaaaacttccacaaatagtttagccaaggggtgacaggtgtgagaataatgtatcgt 346
 Db 269 agaaa-----actaaagcagcgcaagcattaggtctcgcgaagaattgtcaaa 319
 Qy 347 aattaggtaaagcaagtaatgtatatcaacataagctctttttggcactgcattag 406
 Db 320 atgcaataaagccaacactgtatatctgtgcatacctaatttaggtcagattgtg 379
 Qy 407 cgggtatagacttgattcttctaataaaaaggtgatgtgtcactgcattgctc 466
 Db 380 ctggaatgtgattagatgaagccttcagaa---taacagcaacacacagcctctgtca 436
 Qy 467 aagctagttgacttgatgaatgaataattgttaattctatctcagagttacaaagca 526
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 QY 2478 ----ttacaaagtaataaagacagatcaataattgagcactaattgtgtaagatgta 2533
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 QY 2534 gtatatacttcgcgtacaaattgataaaattt 2567
 Db 2528 agcgatcacctcaagaagttgtagtcttat 2561
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 AAV61530
 ID AAV61530 standard; DNA; 2794 BP.
 AC AAV61530;
 XX
 XX
 DT 24-DEC-1998 (first entry)
 DE
 XX
 DE Nucleic acid encoding Leukotoxin 352.
 KW Gonadotropin releasing hormone; GnRH; chimera; leukotoxin polypeptide;
 KW multimer; vaccine; tumour; Leukotoxin 352; LKT 352; Lkta; Plasmid PAA352;
 KW cytotoxic; ss.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2781
 FT /*tag= a
 FT MISC_feature 31..2772
 FT /note= "Encodes recombinant leukotoxin peptide"
 XX
 PN W09806848-A1.
 PD 19-FEB-1998.
 XX
 PF 08-AUG-1997; 97W0-CA00559.
 XX
 PR 09-AUG-1996; 96US-0694865.
 XX
 PA (UWSA-) UNIV SASKATCHEWAN.
 XX
 PI Manns JG, Potter AA;
 DR WPI; 1998-159540/14.
 DR P-PSDB; AAW79568.
 XX
 PT Chimeric protein of leukotoxin and gonadotropin releasing hormone -
 PT useful for, e.g. preparation of vaccines for reduction of incidence
 PT of mammary tumours in mammals
 XX
 PS Disclosure; Figure 3.1-9; 118pp; English.
 XX
 CC The present sequence represents a recombinantly produced or chemically
 CC synthesized nucleic acid encoding leukotoxin 352 (LKT 352), derived from
 CC the lktA gene that is present in the plasmid PAA352. This gene produces
 CC a truncated protein that has an estimated molecular weight of about
 CC 99 kDa and lacks the cytotoxic portion of the molecule. Thus this gene
 CC has a higher expression level than that of the full-length molecule.
 CC This can be used in the construction of a chimeric protein that comprises
 CC a leukotoxin polypeptide, several multimers, and a GnRH sequence. The
 CC chimeric protein can be used as a vaccine to help reduce the incidence of
 CC mammary tumours in a mammalian individual.
 XX
 SQ Sequence 2794 BP; 930 A; 487 C; 599 G; 778 T; 0 other;


```

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Qy      2243 gttctgtgatagtatgaatggtgtgctgtgtaagtgtatgtctatcttcggaag 2302
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Qy      2423 atcatcaggtagatataacataccaagatgtacataacatacaatttaacaaa---- 2477
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Qy      2478 ----ttatcaagtaataaacaagatcataaattgagcaactatgtgtaagaagtta 2533
Db      2468 tgcctattataaagcaactaaagtatgaagaatcgaagaatcgcgtcaaaatgagcg 2527
Qy      2534 gtatatactccgataaattgataaattt 2567
Db      2528 agcgatcactcctcaagaagtgatgactctat 2561

RESULT 11
AAT37176
ID AAT37176 standard; DNA; 2934 BP.
XX
AC AAT37176;
XX
DT 20-NOV-1996 (first entry)
XX
DE LKT-GnRH fusion of PCB113.
XX
KW Leukotoxin; LKT: gonadotropin-releasing hormone; GnRH;
KW fusion protein; immunogen; vaccine; fertility control;
KW contraceptive; sterilisation; plasmid PCB113; ss.
XX
OS Chimeric Pasteurella haemolytica A1 strain B122;
XX
XX Chimeric synthetic.
XX
FH Key Location/Qualifiers
FT 1..2934
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FT /product= LKT-GnRH fusion protein
FT misc_feature 1..30
FT /*tag= b
FT /*note= "vector-derived sequence"
FT 2912..2934
FT /*tag= c
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XX
XX WO9624675-A1.
XX
XX 15-AUG-1996.
XX
XX 24-JAN-1996; 96WO-CA00049.
XX
XX 10-FEB-1995; 95US-0387156.
XX
XX (UUSA-) UNIV SASKATCHEWAN.
XX
XX Manns JG, Potter MA;
XX
XX WPI; 1996-384447/38.

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DR      P-PSDB; AAM03942.
XX
XX Gonadotropin-releasing hormone multimer fusion proteins - with
PT leukotoxin polypeptide for increased immunogenicity, useful in
PT antifertility vaccine prodn.
XX
XX Example 2; Fig 5A-5H; 87pp; English.
XX
XX A chimeric gene fusion (AAT37176) in plasmid PCB113 codes for a
CC fusion protein between a truncated leukotoxin (LKT-352) from
CC Pasteurella haemolytica (see also AAT37179) and a 4-copy
CC gonadoliberin-releasing hormone (GnRH) repeat sequence (see also
CC AAT37178). It was produced by ligating a synthetic sequence for the
CC 4-copy GnRH into vector pAA352 (ATCC 68283), which carries
CC the LKT-352 gene. Recombinant plasmid PCB113 (LKT 352:4 copy
CC GnRH, ATCC 69749) was obtained. Escherichia coli transformants
CC produced the chimeric protein, which is useful as a vaccine for
CC fertility control, partic. in domestic or farm animals.
XX
XX Sequence 2934 BP; 950 A; 529 C; 650 G; 805 T; 0 other;
SQ

```

Query Match 29.3%; Score 814.4; DB 17; Length 2934;

Best Local Similarity 60.2%; Pred. No. 1.8e-170; Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

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Db      29 caaaactggtggcaaaaaattatctctctatctcccaaaattaccatattgactg 88
Qy      107 aaaaagctgggactttaaagatttttaagctgtgtgattgattggtatgctgct 166
Db      89 aacaaagtaatggtttacagatattagtcgaagcgccgaaggttggatgtgagttac 148
Qy      167 tagcagaagagccctacacacgtgaacacgaacaaataactgttgacacagtaaatagt 226
Db      149 aaagaagaagaacgataataattgtcaacagctcaacacagttttaggcagatcaaacg 208
Qy      227 ttctctctcacaacaactgtgattgtctattcttcgacaacaaattgaaagtcttacc 286
Db      209 ctatgtgcttaacgacgtgcgtgtgttattctcgcctcacaacattgataaattgttac 268
Qy      287 aaaaacttccacaataaagttagcacaagaaggttagcaggtgtaaaaattatgatcgta 346
Db      269 agaaa-----actaaagcagccaaagcattaggttcttcgcgaagaagcattgaaag 319
Qy      347 aattaggtaaagcaagtaattgtattatcaaatcaaatgaactcttcttgggacgtgattag 406
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Qy      407 cgggtatagaacttgattctttaacaaaagaagtgatgctgcacgtgatgcttggccta 466
Db      380 ctggaattgatttagatgagcgctctacagaa---taacagcaacacaacactgtcttgta 436
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Db      437 aagctggcttggagctcaacaattcalttaattgaaataatgtccaattcagtaaaacac 496
Qy      527 ttgaagcatttcttcacagtttagcaaaagttagttcttactatatacgcaggtlaaagct 586
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Qy      587 tctctaataatagaacaaagttgcaaaacttaaat---tttctaacaacaaacttggtt 643
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Db      617 tagatgtatctcagggctattatcgcgcgaacagctgcacgtgtlactgtcagataaa 676
Qy      704 atgcacgactggcaaaaagtttgcaggttttgaattgaataagcaatcaatttggta 763
Db      677 atgcttcaacgcctcaaaaagttggtgcggttttgaattgcaaaccaagttgttgta 736

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OY	1883	gtgaacagaagcgggaagttatcacgttaatcgttaaggttgctcgagtgatctacc	1942	
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OY	1943	atgaagttgtgaacgttcaagaacaacgaagttggttaaacgttctaaactacgatac	2002	
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Db	2111	cccttaacggtggtgagatggtgtcgtacatacttgcagtgatacgaacggtcaatgtacgcttat	2170	
OY	2183	ttgggtgtaaaaggcaacgcatacgtcttctlgagaatgaagcgatgatatactcgaatggtcg	2242	
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OY	2534	gtatatcaacttccgaatcgataaatttc	2567	
Db	2528	agcgatcacctccaagaagaatttgatgatttat	2561	
RESULT 12				
ID	AAV61531	standard; DNA; 2934 BP.		
XX	AAV61531;			
XX	24-DEC-1998	(first entry)		
XX	Nucleic acid encoding LKT-GmRH.			
XX	Chimera; pCB113; LKT 352; GmRH; Gonadotropin releasing hormone; multimer;			
KW	cytotoxic activity; antigen presentation; immune response; vaccine;			
KW	tumour; ss.			
XX	Synthetic.			
XX	Key	Location/Qualifiers		
FT	CDS	1...2934		
FT	FT	/*tag= a		
XX				

PN W09806848-A1.
 XX 19-FEB-1998.
 PD 08-AUG-1997; 97WO-CA00559.
 PF 09-AUG-1996; 96US-0694865.
 XX (UYSA-) UNITV SASKATCHEWAN.
 XX
 PA Manns JG, Potter AA;
 PI WPI, 1998-159540/14.
 DR P-PSDB; AAM79569.
 XX
 XX Chimeric protein of leukotoxin and gonadotropin releasing hormone
 PT useful for, e.g. preparation of vaccines for reduction of incidence
 PT of mammary tumours in mammals
 PS Disclosure; Figure 5.1-8; 118pp; English.
 XX
 XX The present sequence represents the nucleic acid encoding the LKT-GnRH
 CC chimeric protein from pCB113. This plasmid contains the LKT 352
 CC polypeptide (AAM79568) fused to four copies of the GnRH peptide. This
 CC chimera lacks cytotoxic activity which enables there to be an increase
 CC in antigen presentation and thus an optimal immune response. The removal
 CC of this region also enables the truncated LKT to be expressed at much
 CC higher levels and allows the amount of antigen administered to be
 CC reduced. This chimeric protein comprises a leukotoxin polypeptide,
 CC several multimers, and a GnRH sequence. The chimeric protein can be used
 CC as a vaccine to help reduce the incidence of mammary tumours in a
 CC mammalian individual.
 XX
 XX Sequence 2934 BP; 950 A; 529 C; 650 G; 805 T; 0 other;
 SQ
 Query Match 29.3%; Score 814.4; DB 19; Length 2934;
 Best Local Similarity 60.2%; Pred. No. 1.8e-170;
 Matches 1536; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

Db 497 ttgaagaaatttgtagagaaattagcaatttggttcaaaactcaaaatacaaaagct 556
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 QY 2423 atcatctcgtatgatttaataacacaaaggtgtaacataacataatcaaaa----- 2477
 Db 2408 gcaaaaaaggaaggtgacatcacaacacgtgtccgagggcgatgttgcgttaagaag 2467
 QY 2478 ----ttatcaaatgaataaaacagatcataaattgacgaactaattggttaagaatgta 2533
 Db 2468 tgcctaatataaagcactaaagaatgagaataatcagaatcatcgtgccaatgtgcg 2527
 QY 2534 gttatacacttcggtcgaatgataaatttt 2567
 Db 2528 agcgatcacctcaaaagcgaattgtagtcttat 2561

RESULT 13

AA054213

ID AA054213 standard; cDNA to tRNA; 3229 BP.

XX AC AA054213;

XX

DF 01-JUL-1994 (first entry)
 XX
 DE Bovine IFNgamma/LKT chimeric gene from plasmid pAA497.
 XX
 KW Bovine; interleukin-2; IL2; P. haemolytica; leukotoxin; LTK; IFN;
 KW ltk; chromosome walking; fusion protein; vaccine; interferon; gamma;
 KW monoclonal; polyclonal; antibody; ds.
 OS Pasteurella haemolytica - chimera.
 OS Bos taurus - chimera.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..3210
 FT /*tag= a
 FT /product= IFNgamma-LKT chimeric protein.
 XX
 PN US5273889-A.
 XX
 PD 28-DEC-1993.
 XX
 PF 22-AUG-1990; 90US-0571301.
 XX
 PR 22-AUG-1990; 90US-0571301.
 PR 16-OCT-1991; 91US-0777715.
 XX
 PA (CIBA) CIBA GEIGY CANADA LTD.
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Campos M, Hughes HPA, Potter A;
 XX
 DR WPI; 1994-006687/01.
 DR P-PSDB; AAR52748.
 XX
 PT Immunogenic fusion proteins of gamma-interferon and immunogenic
 PT leukotoxin - used in vaccines and to raise monoclonal and polyclonal
 PT antibodies
 XX
 PS Claim 3; Fig 7; 56pp; English.
 XX
 CC This sequence encodes a fusion between bovine gamma interferon
 CC (IFNgamma) and Pasteurella haemolytica leukotoxin (LTK). The
 CC leukotoxin gene, ltk, was isolated from a gene library of P.
 CC haemolytica by chromosome walking. Immunogenic fusion proteins
 CC such as this can be used in vaccine compositions. It can also be
 CC used to raise mono- and polyclonal antibodies.
 XX
 SO Sequence 3229 BP; 1085 A; 571 C; 690 G; 883 T; 0 other;

Query Match 29.3%; Score 814.4; DB 15; Length 3229;

Best Local Similarity 60.2%; Pred. No.1.9e-170;

Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

QY 53 caaagctgattaaaaatcttacttctgctatcccaagat-----tatatccgc 106
 Db 29 caaaaactggggcaaaaaattatctctatattcccaaatatccaatgatgactg 88
 QY 107 aaaaagttggactttaaattttaaagttgctgtagaattgattgctcgtt 166
 Db 89 aacaaggtaatggtttcacagatttagtcaagcgccgaagatctggggtcgtgtagc 148
 QY 167 tagcagaagagccatcacactgaaacgcaaaaaaatctgtgacacgaataatcagt 226
 Db 149 aaagagaagaagcaataatattgcaacagctcaaacagtttagcagatccaacgc 208
 QY 227 ttctctctcacacaacactgtagtctattcttctgcacaacaaatagaaaagtcttac 286
 Db 209 ctattgcttaactcagcgtggtgcatgtgtatcgcgtccacaattgataattgtctac 268
 QY 287 aaaaacatttcaacataatgtagcacaaggttagacaggtgtggaataatttatcgta 346
 Db 269 agaaa-----actaaagcagcgcaagcatttagtcttcgcgaagcattgtacaaa 319

OY	347	aactagtgaaagcaagtaatgattatacaacaaactaaagctctcttttttggccactgcatag	406
Db	320	atgcnaataaagcccaaaaactgtattattctatctgcataccaatctatttttagctcatgattg	379
OY	407	cgggtatagaacttgattctcttaataccaanaagtgatgctgcactggttgcttgcta	466
Db	380	cttgaaatggaattttagatgagcgcttaacaga---taacagcaaccaaacatgctcttgcta	436
OY	467	aagctgatattgacttgatttaataatgagataatgtgatatactatccagagtactacaaga	526
Db	437	aagctgcttgtagctaaacaatctatctaatatgaaatatgtgtaattatagtaaaaaaac	496
OY	527	ttgaagcatttctctacagttgacaaagttaggtctctatataatgcagcgtaaaaggt	586
Db	497	ttgcagcaatttctgtagcaaatattgtaatttgcattcaacatacaaaatcatcaagct	556
OY	587	ctctataataggaacaagaattgcaaaactaat---tttcttaaaaaatcttggt	643
Db	557	tagggaactttaggagacaacaactcaaaaataatcgtggaacttgataaagctgcttggt	616
OY	644	tggaataatattacggtcttgtaaccagacttcctgcagcgttcttggttttagcggtataaa	703
Db	617	tagatgttatctccaggctctattatcggtgcagcaacgctgcaacttgacttgtagataaa	676
OY	704	atgcacgacgtgcgaanaaagctgctgcaggttttgaattaaagcaatcaagttatgtgta	763
Db	677	atgcttcaacagcttaaaaaagtgvgcggttttgatttgcaaaccaagtgtytgta	736
OY	764	atgtaacaanaagcaattctctataatgttttagcaaacggtttgctgctgtcatcaa	823
Db	737	ataataccaagaacggttctctctcttaaatatttagccaacggttgcagcaagttatct	796
OY	824	ctactgctgctgctgctgcttaataactcaactcaagttatgttggaactatgctcttgg	883
Db	797	caactggtccctgtagcgtcttaattgcttctactgcttctcttgctgattgcccattag	856
OY	884	catttatgaaatgcagagataaatlcaatcatgctaaatgctcttgatgaatttgcaaac	943
Db	857	catttgcgggtatgtgcggaataaattcaatcatgcaaaaagtttagaggttagtcggac	916
OY	944	aattccgaaaatttggatatgagtgagggaatcatttatgtgctgaatataacgctgtgtg	1003
Db	917	gcttaaaaaaatttaggcatacgacgggaagtaatttattagcaaaatalccgcggggaacag	976
OY	1004	gtactatgaaagcttcaatacacaatattagtaacgcatagtgcaagtttctgtgtgtg	1063
Db	977	ggaactattgatactgcgtgttactgcgaattataacgcgcatitgcgctatgctgtgtg	1036
OY	1064	tttcgcgtgcctgcttagaagctatgctgtgtgtgtgacgcagtgcactatagtttgagtg	1123
Db	1037	tgctctgctgctgcagccggtccggttatgtgtcttcaacggaattgccttatagttcgga	1096
OY	1124	ttacaggaattgactctcgtgaatttagaagcgtcttaaaaggaacatgttttgaagtgtg	1183
Db	1097	ttaccggttgaatttccaaagatctgcgaataatcttaacaagaacaaatgtttgacagctg	1156
OY	1184	ctaacgcttacaaggtaaaatattttagagtgvggnaaagcaaaatcggctgcgaactt	1243
Db	1157	caataaanaatcacaacaaatattgtagaatgggaaaaaataatatacaogtlaagaactct	1216
OY	1244	ttgataaagcgtatgattctcgttatgctgtgcttatttagctaaataactaaatlttgt	1303
Db	1217	tttgaanaatgtttagcagatcccggttactctgcgaatttcaagaagataatagattcttac	1276
OY	1304	cttgcgtcaaaataaaggttggaaagcgtgaacggttatatgcaataccaacaacgttgg	1363
Db	1277	tgaacttaacaagaagtttacaagcgcaagacgtgtcaatctatctatacagaagcaatggg	1336
OY	1364	ataataatcttgatgtttagtcgaggtattaccaaatgttggtlaaacgattlaagacggaa	1423
Db	1337	ataacaacatttgatttagctgctgattagccggttttagtggaanaaagtccttagtgta	1396
OY	1424	aagcttatgcagatgcttlttgaagaatgtaagaagaagttgaagctgtgtcttcaataattact	1483

Db	1397	aagcctatgtagtgcgtttgtaagaagcgcaacacattaaagccgataattagtagcgt	1456
Qy	1484	ttgatgcgtcaaaacgcygatatcatagaccttattgatatccaaatgvggaaaaaacgcgaacgct	1543
Db	1457	ttgatctggcaaacgaagattatttgaatgtagtaattctcgggttaaagcgaaaactctgacata	1516
Qy	1544	tgcatctaacctgcgcttgtttaaagcagaagatbaacaacgttgaagcttcaactatg	1603
Db	1517	tctattcaagaacgcctattatlgcgcgcgggaacagagcatcgttgaacgcytacaacag	1576
Qy	1604	gtlaaataccttataataatgaattaaacttcggaacgtgtlaaaaaacttgcgaattacag	1663
Db	1577	gtaaatatgatatattatcaacaagctcaatatiaacggttagatagctgnaaattacag	1638
Qy	1664	atgagagagctagcttctcaaatatgatttctcctaagtattcaacgctgtacgcgaagacg	1723
Db	1637	atgctgcgcgcaagctctacaccttligattttaaactaacgctgttcacgctattgttattgat	1696
Qy	1724	aaggcacagcagagattgctgtctaagtaatgaatgcaaaa-----g	1762
Db	1697	tagacaatgctcgtgaatagttaactaaacccaagaanaacaaattatgcgaactgtg	1766
Qy	1763	ctgcgaatgcagatatalccttctgttgcctaaagaaatgaaatltgatatgtgtagaattgac	1822
Db	1757	aagtgatgacaaacgtattctgttgctcgtgcagcgcgaatltgattgvcgttagaggt	1816
Qy	1823	acgatcgtgtcttctatagtaagaacggaagattgtgatatcttaccgtagatgtgcga	1882
Db	1817	acgaacccgagttcacattatg---ccgttgaaactatgtgtcttlaactattgtatgaacca	1873
Qy	1883	gtgcacacgaagcagcgagctatatacagtttaacgttaacgttgcctcgaagttgataacc	1942
Db	1874	aagagacccgagcaaggtacgttatataccgttaacgttcttgtagaaacggtlaaagcacatc	1933
Qy	1943	atgaagtgtgtaagcgttcaagaacccaaggttgggtlaaacgtlctgaactaccagttc	2002
Db	1934	acgaagttacttcaaccataccgcatltagtgggcacccgttagaagaanaatagatatac	1993
Qy	2003	gtgattatgattaaagaagaaggttgggtatgattatgaatctacgataatttgaataacg	2062
Db	1994	gtcaatgaacaaataacacgacacatg---ccggttatataccaaaagataactctgaaagctg	2050
Qy	2063	tagaagaagtatcgtgtcttccaaatttaatgatgtatccaaggttccaaattcaacgcgca	2122
Db	2051	ttgaagaataatatactgcgtacatcaacaagatataccttaaaagttagtaagttcaatgtg	2110
Qy	2123	tattccatagtggtgtaagcgtgaatgatttaactcgaatggtgtcgtgtgaacacgcgtgt	2182
Db	2111	cccttaaacggtggtgtagtgcgtacatactatgaactatgaacggaatgaacgcgttat	2170
Qy	2183	ttgtgtgttaagaaggaacgatacgcgacttctcggagatgaagcgatattctgatgtgcg	2242
Db	2171	ttgtgtgttaagaagcgtatgatacttcgcgaatgtgtgtgaatggtgtatgtattctcatgtgcg	2230
Qy	2243	gtctcgtgtgtagatcgtatctaaacgtgtgcgtgtgtatgtatgtcatatcttcggaag	2302
Db	2231	gtlaaagcgaacgactattatacoggtgcggcgaaggtgcgatatcttctgttaacggtlaag	2280
Qy	2303	gtgatgtgaatgatacttvtgtagatgcaacggtgcgaatgtalaatlaagatlttgagaatg	2362
Db	2291	ggcagatgtaatgatatattatcgcgattcttcgaacgcaatgataattatcatcttcgtgt	2350
Qy	2363	caaatatatactgatatatagtattggaacgtataccaagaaggtatattagttaaagcaaat	2422
Db	2351	cgaactttaaagaattttaaactlttgaaaaggttbaaaa---taactgttcatcagata	2407
Qy	2423	atcatcaggtagatattaacataccaagatgtgtgaactaaacataatttacaataa----	2477
Db	2408	gcaaaaaagagaaggtgaccattcaaaaactgtgtccgaagaggtgattttgtctaaagaag	2467
Qy	2478	---ttaaccaagttaaaaacagatcatalaaatltgagcaactaattgttgaagaatgtga	2533

Db 1097 ttacccggtgtaattctcagatcttcgcaatacttcaaacagcaatgtttgacacgttg 1156
 Qy 1184 ctaacccgttcaagagtaaaattttagatgtggaagcaaaatgsggttcagacattt 1243
 Db 1157 caataaattcattacaacaaattttagaatggaagaaataaataacgtgtaagaactt 1216
 Qy 1244 ttgataaagctatgattctcgttatgctgttatttagactaactaaattttgt 1303
 Db 1217 ttgaaaatggtttagatgcccgttattcttgcaatttcaagataataatgaaattttac 1276
 Qy 1304 ctgagcttaataaagagttgaagctgaacgtgttattgcaatacccaacaacgttgg 1363
 Db 1277 tgaacttaaacaaagatttacaagcgaaacgttgcattctacttaagaagaatgg 1336
 Qy 1364 ataataatattggtgagttacaggtattacaaatttggtggaacgcaataagaacgaa 1423
 Db 1337 ataacaacattggtgattttagctgttatagccgttttagtggaagaaagctccttggta 1396
 Qy 1424 aagcttatgcaatgcttttgaagatggaagaaagtgaagctgtgttccaataattt 1483
 Db 1397 aagcctatgtgattgctgtttgaagaagcaaacatttaagccgataaatttagtaacgt 1456
 Qy 1484 tggatgtcaaacactggtatctatagacattagtaattcaaatgggaaaaaacgcaagct 1543
 Db 1457 tggattcggcaaacggtatttattgtatgtgaaattcgggtlaaagcgaaacctacata 1516
 Qy 1544 tgcatttactcgccttgttlaacagcagaactgaatcgcgtgaacgtttaactaatg 1603
 Db 1517 tctatttcagaacgcctattttagcgcgggaacagacacgtggaacgttacaacag 1576
 Qy 1604 gtaataactcttataataaagttaaaatcgcgaactgttaaaaaactgcaagttacag 1663
 Db 1577 gtaaatatgaaataattacacagctcaaatlaaacggttagatagctggaataattacag 1636
 Qy 1664 atggaagagcaggtctcaaatatagattcttcaagatttaccggtttagccgagacag 1723
 Db 1637 atgtgtcagcagacttctacacttatttaactaacgttgcacggttattgttgaat 1696
 Qy 1724 aagcacaagcagatgtgtctaatagtaaatgcaaaa-----g 1762
 Db 1697 tagacaatgtcgtgaatgttaactaaacaaagaacaaataatttccaaactgtgt 1756
 Qy 1763 ctggcaatgacgatatcttgttgcgaagtaaatgaaatgaaatggtggaatgac 1822
 Db 1757 aaggtgtatgaaacgtatttctgttctgttgcacggaataatgatggcgttgaagtt 1816
 Qy 1823 acgactgtcttcttataagtaagaagcgaagattgtggaatattacgttagatgtgaca 1882
 Db 1817 acgacgagttcactataag---ccgtggaactgtgtgttacttactatgtatgacaaca 1873
 Qy 1883 gtgcacaagaagcagcaggtatatacagtttaactglaaggttgcgaggtatattctacc 1942
 Db 1874 aagagaccgagcaaggtatgataacgtlaactgttgcgtaagaacggtlaaagcactac 1933
 Qy 1943 atgaagttgtgaaagcgtcaagaacaaagtggttaaacgtaactgaaactccaagtatc 2002
 Db 1934 acgaagtgtacttcaaccataccgcatatgtggtcaacccgtgaagaaaaaatagaatac 1993
 Qy 2003 gtgatttgaatgaagaaagtgtgtatgttgcagttacgcgaataatttgaatacag 2062
 Db 1994 gtctatacataaacacagacatg---ccgttattacacaaagaataacttgaagaactg 2050
 Qy 2063 tagaagaagttaattggttctcaatttaagtattcaatgaagttcaatcaacagaca 2122
 Db 2051 ttgagaagaattatgtctacacataacagatatctttaaaggtagtaagttaacatgattg 2110
 Qy 2123 tatcccatagtggtgaaaggtgataatttactcagtggtgtgctggtggaacgcctgtt 2182
 Db 2111 cctttaaagtggtgagtggtgcatactattgacggtlaaagcgaatgcaatgccttatt 2170
 Qy 2183 ttggtgttaagcgaacgacttctctgagatgaaagcgaatgatttactcagatggcg 2242

Db 2171 ttggtgtaaagcgatgatatactcgaatgtgtggaatgtgatttatacgtatgcg 2230
 Qy 2243 gtctcgtgtagatgatataatgtgtgtgtgtgaatgagttatatactttggaaag 2302
 Db 2221 gtaaaagcaagcactattacaacgttgcgaaggtgagatatttctgttccacgtlaag 2290
 Qy 2303 gtgattgtaatgatacttctgtcagatggaacggtgaatgataaattagcatttgcagatg 2362
 Db 2291 ggaatgtaatgataatttactcagattctgacgcaatgaaataattatcattctctgtt 2350
 Qy 2363 caataatactgataatttgaattgaacgttaccagaagaggtattatagttaaacgaatg 2422
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 Qy 2423 atcattcaggtagatttatacacaagatgtgtacataacataaatttacaana----- 2477
 Db 2408 gcaaaaaagaaagatgaccccttcaaaactgttccggaagcgtgattttctaagaag 2467
 Qy 2478 ----tlatcaaaagtaataaacaagatcataaaattgagcaactaattgtlaaagatgta 2533
 Db 2468 tgcctaatattaaagcaactaagaatgagaataatcgaagaataatcgtgtcaaatggtcg 2527
 Qy 2534 gttatattcacttcgattcaaatgtataaattt 2567
 Db 2528 agcgaatcactcaagcaagttgattcttat 2561

RESULT 15
 AAN72484
 ID AAN72484 standard; DNA; 3229 BP.
 AC AAN72484;
 XX 19-DEC-2000 (first entry)
 DT
 DE Bovine gamma-IFN/Pasteurella haemolytica leukotoxin fusion gene.
 XX
 KW Bovine gamma-IFN; gamma-Interferon; leukotoxin; LKT; respiratory disease;
 KW pneumonia; shipping fever; cattle; livestock; anti-Pasteurella vaccine;
 KW immunogen; ds.
 OS Chimeric - Bos taurus.
 OS Chimeric - Pasteurella haemolytica.
 OS
 XX
 FH Location/Qualifiers
 FT CDS 1..3297
 FT /*tag= a
 FT /product= "Bovine gamma-IFN/Pasteurella haemolytica
 FT leukotoxin fusion protein".
 FT
 PN US6096320-A.
 XX
 PD 01-AUG-2000.
 XX
 PF 20-OCT-1997; 97US-0954418.
 XX
 PR 20-DEC-1993; 93US-0170126.
 PR 22-JUL-1996; 96US-0681479.
 PR 22-AUG-1990; 90US-0571301.
 PR 16-OCT-1991; 91US-0777715.
 XX
 PA (UWSA-) UNIV SASKATCHEWAN.
 PA (CIBA) CIBA GEIGY CANADA LTD.
 PI Campos M, Hughes HPA, Potter A;
 XX
 DR WPI, 2000-531543/48.
 DR P-PSDB; AAB21074.
 XX
 PT Vaccine for stimulating immunity against pneumonia comprises chimeric
 PT protein comprising gamma-Interferon and leukotoxin derived from
 PT Pasteurella haemolytica -
 XX

QY 1863 gtgcacagaagcgagcaagttatacagtttaacgttaaggttgctcgaggtgatatctacc 1942
Db 1874 aagagaccgagcaagtagttataccgttaacgttttcgtagaacccggtaaagcactac 1933
QY 1943 atgaagttgtgaagcggtcaagaacccaaggtgggttaaacgfractgaactaccagttac 2002
Db 1934 acgaagtgactccaaccatccgcatcattagtggtgaacccggtgaagaaaaataaatatc 1993
QY 2003 gtgtatcgaattgaagaagttggtatgtgtatcagttcagtcgaataattgaatcag 2062
Db 1994 gtcatagcaataacaccgacacatg---ccggttattacaccaagaatataccttgaaagctg 2050
QY 2063 tagaagaagtaattgtgtctcctaatttaagtatgtattcaaaaggttctaattcaagaca 2122
Db 2051 ttgaagaattatcgttatacacaatacgaatattttaaaggttaagttacgttcaatgtg 2110
QY 2123 tattccatagttgtgaaggtgaattgaattactcgatggtggtgtgtgaacgacgctgt 2182
Db 2111 ccttaacggtgtgtatgtgtgtcgatctactatgtacggtgaacgcaatgacgcttat 2170
QY 2183 ttgtgtgtgaagcgacgacgtacttctgtgaatgaagcgatgattactcgatggtg 2242
Db 2171 ttgtgtgaagcgatgattctcgatgtgtggaatggtatgtatttactcgatggtg 2230
QY 2243 gtctgtgtatgtatgtatgaatgtgtgtgtgtgaatgtgtatcttctcgaaag 2302
Db 2231 gtcaagcgcaacgacctatcaacggtgcaagcgatgatatcttctgtaacgtaag 2290
QY 2303 gtgatgtgaatgtatacttgtacgaatgcaagcggaatgataatgaatgtgcatg 2362
Db 2291 gcgatgtgaatgtataattacccgattctgaacgcaatgataatataatctctgatt 2350
QY 2363 caaatatctgatatgtatgtgaacggtacccaagaggttataagttaaagcaatg 2422
Db 2351 cgaacttaaaagatttaacattgaaaagttaaca---taacttgcatacagaata 2407
QY 2423 atcaatcaggtatgaatacacaagaatgtgtacataacacatcaaatthacaaa----- 2477
Db 2408 gcaaaaaagagaagtgacacatccaactggttccgagaggtgatttgcataagaag 2467
QY 2478 ----ttatcaaaagtaataaacaagatcatataaattgagcaactaattgtgaagatgta 2533
Db 2468 tgcctaattataaagaactaagaatgagaataatcgaagaataatcaggtcaaaatggtg 2527
QY 2534 gttatatacttccgatacaaatgtataaattt 2567
Db 2528 aacggtatcacctcaagaagttgatgatctat 2561

Search completed: September 15, 2002, 11:57:09
Job time: 10587 sec

SCOT D

RESULT 4
AAR10889
ID AAR10889 standard; Protein: 924 AA.
XX
AC AAR10889;
XX
DT 11-APR-1991 (first entry)
XX
DE Leukotoxin 352 encoded by plasmid PAA352.
XX
KM LKT; vaccine: antigen; respiratory disease; shipping fever pneumonia.
XX
OS Pasteurella haemolytica A1 strain B122.
XX
PN CA2014033-A.
XX
PD 07-OCT-1990.
XX
PF 06-APR-1990; 90CA-2014033.
XX
PR 07-APR-1989; 89US-0335018.
XX
PA (UTSA-) UNIV SASKATCHEWAN.
XX
PI Acres SD, Babluk LA, Potter AA, Lawman MJF.
XX
DR WPI: 1991-000097/01.
XX
N-PSDB: AAO10272.
XX
PT Pasteurella haemolytica proteins and genes - used for producing
XX
PT vaccines to protect animals esp. cattle from respiratory diseases
XX
e.g. pneumonia.
XX
PS Claim 13; Fig 5; 87pp; English.
XX
CC Plasmid PAA352 is derived from PA114, a clone isolated from a
XX
CC genomic library of P. haemolytica. The protein, designated "new
XX
CC leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin.
XX
CC LKT 352 and pref. antigenic fragments of it, can be used in
XX
CC vaccines to protect cattle from respiratory diseases. They can also
XX
CC be used to produce antibodies for immunofluorescence purification.
XX
CC See also AAR10890, AAR10909, AAR10910 and AAO10783.
XX
CC
XX
SO Sequence 924 AA;
Query Match 75.4%; Score 43; DB 12; Length 924;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FLSELNKELEAE 12
DB 422 fllnlknlqae 433

RESULT 6
AAR42380
ID AAR42380 standard; Protein: 924 AA.
XX
AC AAR42380;
XX
DT 19-APR-1994 (first entry)
XX
DE Recombinant leukotoxin peptide (split) from plasmid pGCN4.
XX
KM Haemophilus somnus; immunogenic; haemolysin: lppB; lppC;
XX
KM thromboembolic meningoencephalitis; septicemia; arthritis;
XX
KM pneumonia; lktA gene; haemin-binding protein; fusion protein.
XX
OS Pasteurella haemolytica.
XX
PN WO9321323-A.
XX
PD 28-OCT-1993.
XX
PF 05-APR-1993; 93WO-CA00135.
XX
PR 09-APR-1992; 92US-0865050.
XX
PR 04-JUN-1992; 92US-0893424.
XX
PR 04-JUN-1992; 92US-0893426.
XX
PR 29-MAR-1993; 93US-0038287.
XX
PR 29-MAR-1993; 93US-0038288.
XX
PR 29-MAR-1993; 93US-0038719.
XX
PA (UTSA-) UNIV SASKATCHEWAN.
XX
PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
XX
PI Rioux C, Theisen M;
XX
DR WPI: 1993-351733/44.
XX
N-PSDB: AAO1086.
XX
PT Haemophilus somnus immunogenic proteins used in vaccines -
XX
PT selected from haemin-binding protein, haemolysin, lppB and lppC,
XX
PT and corresp. DNA
XX
PS Disclosure; Fig 11; 119pp; English.
XX
CC The lppB gene protein was expressed in E. coli as a fusion to the
XX
CC Pasteurella haemolytica leukotoxin gene lktA coded for by plasmid
XX
CC PAA352. The lppB gene fragment was taken from pMS11. lppB can be
XX
CC used in vaccines for preventing or treating H. somnus infections;
XX
CC which cause thromboembolic meningo-encephalitis, septicemia, arthritis
XX
CC and pneumonia in vertebrates.
XX
CC See also AAR42370-86.
XX
XX
SO Sequence 924 AA;
Query Match 75.4%; Score 43; DB 14; Length 924;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FLSELNKELEAE 12
DB 424 fllnlknlqae 435

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2002, 22:25:42 ; Search time 2862.36 Seconds
(without alignments)
13127.462 Million cell updates/sec

Title: US-09-884-696-1

Perfect score: 2784

Sequence: 1 atgccaataataatgtat.....tttggcccaagtgttag 2784

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estdb:*
2: em_esthm:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123.2	4.4	450	12	AF307787 AF307787
2	109.6	3.9	463	12	AF307788 AF307788
3	82.4	3.0	908	12	AZ548467 ENTKE30TR
4	79.8	2.9	843	12	AZ551618 ENTIDV54TR
5	78.8	2.8	877	12	AZ531291 ENTBO34TR
6	78.2	2.8	912	12	AZ551092 ENTFCJ22TR
7	74.8	2.6	849	12	AZ546009 ENTFC53TR
8	73.6	2.6	726	12	AZ196050 SP_1031_A
9	73.2	2.6	905	12	AZ550256 ENTVE58TR
10	72.2	2.6	976	12	BH149983 ENTOD93TR
11	71	2.6	582	12	CNS0173R Tetraodon
12	70.4	2.5	795	12	AZ528485 AL166032 Tetraodon
13	70.4	2.5	833	12	AZ676218 ENTKE36TR
14	70.4	2.5	843	12	BH139532 ENTNG88TR
15	70.4	2.5	931	12	BH160272 ENTQV49TR
16	66.8	2.4	816	12	AZ535744 ENTQ25TR
17	66.6	2.4	900	12	AZ549980 ENTDD94TR

C	18	65.4	2.3	1101	12	CNS0039G	AL063921 Drosophila
C	19	65	2.3	891	12	AZ683582	ENTKK47TR
C	20	64.8	2.3	866	12	CNS02C24	AL180587 Tetraodon
C	21	64	2.3	358	10	BH170666	BH170666 EST573189
C	22	64	2.3	605	10	BH163520	BH163520 EST566043
C	23	64	2.3	747	10	BH162732	BH162732 EST565255
C	24	64	2.3	943	12	AZ211711	AZ211711 SP_0157_B
C	25	63.6	2.3	479	12	BH211305	BH211305 SMI_50G32
C	26	63.6	2.3	794	10	BH159906	BH159906 EST562429
C	27	63.4	2.3	774	12	CNS02A2C	AL188841 Tetraodon
C	28	63.4	2.3	890	12	AZ530768	AZ530768 ENTBH54TR
C	29	63.2	2.3	487	12	BH200321	BH200321 SMI_50O20
C	30	63	2.3	474	9	BE059711	BE059711 sn35h05_Y
C	31	63	2.3	717	10	BH160500	BH160500 EST563023
C	32	62.4	2.2	541	12	AQ242166	AQ242166 1E13-28C
C	33	62.4	2.2	838	10	BG535503	BG535503 602563188
C	34	62.4	2.2	880	12	AZ669474	AZ669474 ENTIV88TR
C	35	62.2	2.2	550	12	AQ403310	AQ403310 HE_5061_B
C	36	61.8	2.2	476	10	BH566802	BH566802 UT-R-BJ06
C	37	61.8	2.2	548	12	BH200391	BH200391 SMI_39D16
C	38	61.8	2.2	906	12	BH153606	BH153606 ENTTS83TR
C	39	61.8	2.2	1101	12	CNS0106X	AL098595 Drosophila
C	40	61.6	2.2	824	12	BH396872	BH396872 AG-ND-101
C	41	61.4	2.2	548	10	BH159818	BH159818 EST562341
C	42	61.4	2.2	810	12	CNS0272N	AL184136 Tetraodon
C	43	61.2	2.2	645	10	BH165350	BH165350 EST567873
C	44	61	2.2	815	12	BH356455	BH356455 C1230-163
C	45	60.6	2.2	493	10	BH170559	BH170559 EST573082

ALIGNMENTS

RESULT 1
AF307787
LOCUS AF307787 Escherichia coli CF073 Escherichia coli genomic clone
DEFINITION 2b11-593, DNA sequence.
ACCESSION AF307787
VERSION AF307787.1 GI:12250177
KEYWORDS GSS.
SOURCE Escherichia coli.
ORGANISM Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
REFERENCE 1 (bases 1 to 450)
AUTHORS Bahranl-Mougeot,F.K., Pancholl,S., Daoust,M. and Donnenberg,M.S.
TITLE Identification of putative urovirulence genes by subtractive cloning
JOURNAL J. Infect. Dis. (2001) In press
COMMENT Contact: Bahranl-Mougeot, FK
Department of Medicine-Division of Infectious Diseases
University of Maryland
MSTF Rm 9.00 -10 S. Pine St., Baltimore, MD 21201, USA
Tel: 410-706-7560
Fax: 410-706-8700
Email: fbahranl@umaryland.edu
Class: unknown.
Location/Qualifiers
1. 450
/organism="Escherichia coli"
/strain="CF073"
/db_xref="taxon:562"
/clone="2b11-593"
/note="Escherichia coli CF073"
/note="uropathogenic; isolated based on subtractive hybridization with Escherichia coli K12; putative urovirulence genes"
BASE COUNT 142 a 61 c 122 g 121 t 4 others
ORIGIN
Query Match 4.4%; Score 123.2; DB 12; Length 450;

[illegible]

RESULT	2
LOCUS	AF307788/c
DEFINITION	AF307788 Escherichia coli CFT073 linear GSS 17-JAN-2001
ACCESSION	AF307788
VERSION	AF307788
KEYWORDS	AF307788.1 GI:12250179
SOURCE	GSS.
ORGANISM	Escherichia coli.
REFERENCE	Escherichia coli.
AUTHORS	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
TITLE	1 (bases 1 to 463)
	Bahnani-Mougeot,F.K., Pancholi,S., Daoust,M. and Donnenberg,M.S.
	Identification of putative urovirulence genes by subtractive

**JOURNAL
COMMENT**
J. Infect. Dis. (2001) In press
Contact: Bahrani-Mousset FK
Department of Medicine-Division of Infectious Diseases
University of Maryland
MSTF Rm 9 00-10 S. Pine St., Baltimore, MD 21201, USA
Tel: 410-706-7560
Fax: 410-706-8700
Email: fdbahrani@umaryland.edu
Class: unknown.

FEATURES	source
Location/Qualifiers	
1. .463	
/organism="Escherichia coli"	
/strain="CPT073"	
/db_xref="taxon:562"	
/clone="2b11-594"	
/clone_11b="Escherichia coli CPT073"	
/note="uropathogenic; isolated based on subtractive hybridization with Escherichia coli K12; putative urovirulence genes"	
BASE COUNT	123 a 130 c 62 g 146 t 2 others
ORIGIN	

Query Match	3.9%;	Score 109.6;	DB 12;	Length 463;
Best Local Similarity	58.1%;	Pred. No. 4.4e-12;		

Matches 230; Conservative 0; Mismatches 161; Indels 5; Gaps 2.

Oy	1921	gttcttcgagtgatgattctaccatgaattctggaagcgctcaagaacccaagtggtgtaa	1980
Db	461	GGTGCTATCTTAAAGCTATTTTACAGGAAGTTG-NAAGGAGCAGNNAGTTTCAGTTGGAAA,	403
Oy	1981	cyctactgaactatccagiatcgtgattatgaat---taagaaagtctggtatggtta	2036
Db	402	AGAACTGAAMAAAGCAATATGGAGATTATGATTCACCTCATTCATCAATGTGAAMAAATTTA,	343
Oy	2037	tcagctaacgataatttgaatcagtagaagaagtaatttgcttcctcaatttaagtgt	2096
Db	342	CCAGAGACTTGATTAACCTATATATCCCTGGAMAACTTTATTTGGAGCCAGCGCTGGCGCAA	283
Oy	2097	attcaaaagttctaaattcaacagacatcatccatagctggtgaagtgatgaattaacgta	2156
Db	282	GTTTTTTGGCAGTAATTTACTGATATCTTCCATGGCGCGGATGTGTATGACCATATAGA	223
Oy	2157	tgtgtgctcgtgtgaacagccgcttgcttggttggtlaaagacaagatcgaacttctgaga	2216
Db	222	AGGAATATGATGGGATATCCGCTTATATATGATTAAGGTATATGATATGATGCGTGAGGGCGG	163
Oy	2217	tgaagcgagatgattactcgatagtggtgctctgtgtgatgatagtattaaatggtgtgtg	2276
Db	162	AAAGGGGAGTAGCACGCTCTATGGCGGTATGGCAATGTATTAATTATGGGGGACAGG	103
Oy	2277	taatgatgtctatattcttcgaaagtgatgtaa	2312
Db	102	TATATATTACTTTACGCGGCTACGAGATATATGA	67

RESULT 3
A7548467

LOCUS	908 bp	DNA	linear	GSS_14-NOV-2000
AZ548467				
DEFINITION	Entamoeba histolytica	Sheared	DNA	Entamoeba histolytica
	genomic, DNA sequence.			

ACCESSION	AZ548467	
VERSION	AZ548467.1	GI:11172102
KEYWORDS	GSS.	
SOURCE	Entamoeba histolytica.	
ORGANISM	Entamoeba histolytica	

REFERENCE	Eukaryota; Entamoebidae; Entamoeba.
AUTHORS	1 (bases 1 to 908)
TITLE	Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library
JOURNAL	Unpublished (2000)
COMMENT	Contact: Brendan J Loftus

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the *Entamoeba histolytica* HM1:IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: Shotgun
High quality sequence start: 17
High quality sequence stop: 828.

FEATURES	location/qualifiers
source	1. .908

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/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/cb_xref="taxon:5759"
/clone_id="Entamoeba histolytica Sheared DNA"
/vector="PHOS1; Site 1; Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broch cultures of E. histolytica
using a method described by Clark and Diamond (Clark
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a

```


JOURNAL COMMENT

Unpublished (2000)
 Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: bjlloftus@tigr.org
 Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
 Seq primer: M13-Forward
 Class: shotgun
 High quality sequence start: 17
 High quality sequence stop: 861.
 Location/Qualifiers

FEATURES

1..912
 Location/Qualifiers

/organism="Entamoeba histolytica"
 /strain="HMI:IMSS"
 /db_xref="taxon:5759"
 /clone_lib="Entamoeba histolytica Sheared DNA"
 /note="Vector: pHOSt; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999)."

BASE COUNT 423 a 34 c 264 g 191 t
 ORIGIN

Query Match

Best Local Similarity 2.8%; Score 78.2; DB 12; Length 912;
 Matches 311; Conservative 0; Mismatches 388; Indels 0; Gaps 0;

QY 1631 aattcgagcgtgtaaaactgcaagttacagatgagagcgtacttaattagatt 1690
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 202 AATTAGAGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATG 261
 QY 1691 tctctaagttatcagcgtgttagcgcagacagagcagacagcagattggtctaa 1750
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 262 ATGATGAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 321
 QY 1751 taatgcaaaagctggcaatgacgatattcttggccaaggtaaataatgattg 1810
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 322 ATGATGAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 381
 QY 1811 gtggagatgacacgactcgtctctctatagtaaaagcggagagattggttaatactg 1870
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 382 AAGACGACGAATTTGAATTGAAGATGATGATGATGATGATGATGATGATGATG 441
 QY 1871 taagatgaagagtgcaacagagcaggtatacagtttaactgtaaggttgcagag 1930
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 442 ATGATGAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 501
 QY 1931 gtgatatctaccatgagtggtgaaagcgtcaagaacaaaggtggttaacgttaactgaa 1990
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 502 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 561
 QY 1991 ctatccagttatcgtatgtaataaagaagttgggtatggttalcagttctaccgata 2050
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 562 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 621
 QY 2051 atttgaatcagtagaagaagattggtctcctaattatgattatcctaaggtctcta 2110
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 622 ATGAAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 681

QY 2111 aattcaacgacatatccatagttgtagaagtgatgattactcagatggtgtgtcgtg 2170
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 682 ATGATGAGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 741

QY 2171 acgacccgtgttggtagaaagcagacgcacttcttgagatgaagcgatgatt 2230
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 742 ATGAAGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 801

QY 2231 tactcgatgagcgttctggtgtatgtatataatgtgtgtgtgtatgtatctcta 2290
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 802 AAGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 861

QY 2291 tcttcgaaagtgatgtagtaatacttctgtagcgtg 2329
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 862 ATGAATTTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 900

RESULT 7

AZ546009/c 849 bp DNA linear GSS 14-NOV-2000

LOCUS ENTPE53TF Entamoeba histolytica Sheared DNA Entamoeba histolytica

DEFINITION genomic, DNA sequence.

ACCESSION AZ546009

VERSION AZ546009.1 GI:11167130

KEYWORDS GSS.

SOURCE Entamoeba histolytica.

ORGANISM Entamoeba histolytica.

REFERENCE 1 (bases 1 to 849)

Loftus, B., Van Aken, S. and Fraser, C.
 Determination of clone end sequences from Entamoeba histolytica

HMI:IMSS sheared DNA library

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: bjlloftus@tigr.org
 Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
 Seq primer: M13-Forward
 Class: shotgun
 High quality sequence start: 26
 High quality sequence stop: 796.
 Location/Qualifiers

FEATURES

source

1..849
 Location/Qualifiers

/organism="Entamoeba histolytica"
 /strain="HMI:IMSS"
 /db_xref="taxon:5759"
 /clone_lib="Entamoeba histolytica Sheared DNA"
 /note="Vector: pHOSt; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999)."

BASE COUNT 199 a 236 c 43 g 371 t
 ORIGIN

Query Match

Best Local Similarity 2.7%; Score 74.8; DB 12; Length 849;
 Matches 244; Conservative 0; Mismatches 282; Indels 0; Gaps 0;

FEATURES
source

Location/Qualifiers
1. 905
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: PHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."

BASE COUNT 203 a 260 c 46 g 396 t
ORIGIN

Query Match 2.6%; Score 73.2; DB 12; Length 905;
Best Local Similarity 45.1%; Pred. No. 0.00012;
Matches 313; Conservative 0; Mismatches 378; Indels 3; Gaps 1;

QY 1674 tagttctaaattgattctctcctaagtatcagcgtgtgacgagacagaagcagaca 1733
DB 883 TATTCAATTTGTTGCACTTATTACTACTGCTTCGCGAAGATTCTTTCATGAC 824
QY 1734 cgaagcttggtctaatgataatgcaaaagctgacgaatgatactcttggtgcaag 1793
DB 823 TGAATAATGTAAGAAATGCAACATCAATACCACTTGAAGAACAAATTAACAGACATGA 764
QY 1794 taaatgaaatgatgattgattgattgacacgattgattctctctatagaagaacgagga 1853
DB 763 TCATGATGAAATTTGAAATTTAGACAGCAAGATGATGATGATGATGATGATGATGATG 707
QY 1854 atttgtaataatactgtagatgtagacagatgcaacagaacgagcaggtatcaagttaa 1913
DB 706 AGATGAGAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 647
QY 1914 tcgtaagattgctcgaagtgatatactaccatgaagttgtaagcgttcagaagaacccaaggt 1973
DB 646 ATTGAAAGATGAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 587
QY 1974 gggtaaacgtactgaaactatccagatcgtgattgaattgaagaagaattggtatgg 2033
DB 586 TGATGAAGATGAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 527
QY 2034 ttatcgctctaccgaataattgaaatcagtagaagaagaattggtctcctaatttaatga 2093
DB 526 ATTTGAAATTAAGAAGATGAGAAGATGAGAAGATGAGAAGATGATGATGATGATGATG 467
QY 2094 tggatccaagaaggtctcaaatccaacacatccatagtggtggaagtgatcttact 2153
DB 466 AGATGATGAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 407
QY 2154 cgaatggtggtcgtgtagacagccgctgtttggtggtgaaagaacagatcgaatcttctg 2213
DB 406 TGATGAAGATGAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 347
QY 2214 agatggaagcgaatcttactcgaatggtggtgtctggtgtagatgatttaaaatggtgtgc 2273
DB 346 AGATGATGATGAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 287
QY 2274 tggtaatgattgctctatactcttcggaagaagtgtagtaagattcttgcacatggtgac 2333
DB 286 TGAAGATGAGAAGATGAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 227
QY 2334 gggcaatgataaattgacattgacagatgcaat 2367

DB 226 TGAAGATGAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 193

RESULT 10
LOCUS BH149983 976 bp DNA linear GSS 27-AUG-2001
DEFINITION ENTQD93JF Entamoeba histolytica sheared DNA Entamoeba histolytica genomic, DNA sequence.
ACCESSION BH149983
VERSION BH149983.1 GI:15311165
KEYWORDS GSS.
SOURCE Entamoeba histolytica.
ORGANISM Entamoeba histolytica
REFERENCE 1 (bases 1 to 976)
AUTHORS Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
TITLE Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library (2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b1loftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
Seq primer: M13-Forward
Class: Shotgun
High quality sequence start: 38
High quality sequence stop: 740.

FEATURES
source
Location/Qualifiers
1. 976
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: PHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."

BASE COUNT 415 a 63 c 280 g 218 t
ORIGIN

Query Match 2.6%; Score 72.2; DB 12; Length 976;
Best Local Similarity 44.0%; Pred. No. 0.0002;
Matches 305; Conservative 0; Mismatches 388; Indels 0; Gaps 0;

QY 1739 ttggtcctaagtaaatgcaaaagctgcaatgacgaatattctgttgcgaagtaaaa 1798
DB 89 TTGCTTAATTTCTTAACGTCTTCATGCGCAAGAGATTGAACCTGCATGATGATTTTGAAA 148
QY 1799 tgaatattgattggtggaatggaacagatcgtgtctctatagtaagaacgaggaatttg 1858
DB 149 TTAATAATGAAGATTTGATTTTAATGATGATGATGATGATGATGATGATGATGATGATG 208
QY 1859 gtaatactgtagatgtagacaggttgcaacagaagcgaatgataagatttaacgtta 1918
DB 209 ACGACGATGATGATGATGATTTGAAATTTAGACAGCGAAGAAAGATGATGATGATGATG 268
QY 1919 aggttgcgcgtgtagatactaccatgaagtttggaagcgtcgaagaacaaagtggtga 1978

Db 269 AAGTGAAGAAGAGATGAGAGAGAGATGAAGAAGATGAAGAAGATGATG 328
Qy 1979 aagtaactgaacatccatccatcgtatcgtatcgtatcgtatcgtatcgtatc 2038
Db 329 AAGAAGACGATGATGAAGAAGACGATGATGAAGAAGACGATGATGATG 388
Qy 2039 agctaccgataatcttgaatcgaatgaagaagatcgttgcataatgaatgat 2098
Db 389 AAGAAGACGATGATGAAGAAGACGATGATGAAGAAGACGATGATGATG 448
Qy 2099 tcaaaagttcctaatacgaacatcctcagtagtgtagtgtagtgtagtgtag 2158
Db 449 AAGAAGACGATGATGAAGAAGACGATGATGAAGAAGACGATGATGATG 508
Qy 2159 gt 2218
Db 509 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 568
Qy 2219 aagcgaatgattactcgtatcgtatcgtatcgtatcgtatcgtatcgtatc 2278
Db 569 AAGAAGATGATGATGAAGAAGATGATGATGAAGAAGATGATGATGAAGAAGATG 628
Qy 2279 atgattctatactcttcggaagtgtagtgtagtgtagtgtagtgtagtgtag 2338
Db 629 ATGAAGAAGATGATGAAGAAGATGATGAAGAAGATGATGAAGAAGATGATG 688
Qy 2339 atgataatgacattcgtacgaatcgaatcgtacgaatcgtacgaatcgaat 2398
Db 689 ATGATGATGAAGAAGATGATGATGATGATGAAGAAGATGATGAAGAAGATG 748
Qy 2399 aggtattatagtttaacgaatgatcattcag 2431
Db 749 ACGATCGAGATGACGATCGAGATCGAGATCGAGATGAG 781

RESULT 11
CNSO1T3R/c 582 bp DNA linear GSS 12-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 194G01 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL166032.1 GI:7803770
VERSION GSS: genome survey sequence.
KEYWORDS Tetraodon nigroviridis.
SOURCE Tetraodon nigroviridis.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorphi; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 582)
Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 582)
Roest-Crollius,H., Jallion,O., Dasilva,C., Bonneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 582)
Genoscope.
TITLE Direct Submission
AUTHORS Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
JOURNAL This sequence is a single read and was generated as part of a large
COMMENT scale clone-and-sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
Location/Qualifiers

source 1. 582
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone_1lb="G"
/clone_1lb="G"
/note="Genoscope sequence ID : C0AG194AD01LPI-end : T7"
BASE COUNT 165 a 197 c 95 g 117 t 8 others
ORIGIN

Query Match 2.6%; Score 71; DB 12; Length 582;
Best Local Similarly 58.0%; Pred. No. 0.00031;
Matches 119; Conservative 3; Mismatches 83; Indels 0; Gaps 0;

Qy 2129 atagtgtagagtgtagttagttagttagttagttagttagttagttagttagttag 2188
Db 468 ATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 409
Qy 2189 gtaaggaacagatcgacttcggaagatgaagagcagatgattactcgtatcgt 2248
Db 408 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 349
Qy 2249 gtgattgtgatttaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2308
Db 348 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 289
Qy 2309 gtaatgacttctgtagatgtagc 2333
Db 288 TTGGAGGTTGTTTTCGCTGAGAC 264

RESULT 12
A2528485 795 bp DNA linear GSS 03-NOV-2000
LOCUS Entamoeba histolytica
DEFINITION ENT64TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, DNA sequence.
ACCESSION A2528485
VERSION A2528485.1 GI:11080747
KEYWORDS GSS.
SOURCE Entamoeba histolytica.
ORGANISM Eukaryota; Entamoebidae; Entamoeba.
REFERENCE 1 (bases 1 to 795)
Loftus,B., Van Aken,S. and Fraser,C.
AUTHORS Determination of clone end sequences from Entamoeba histolytica
TITLE HMI:IMSS Sheared DNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Forward
Class: Shotgun
High quality sequence start: 23
High quality sequence stop: 790.
FEATURES
Location/Qualifiers
1. 795
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_1lb="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOSt1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a

light size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999)."

BASE COUNT 319 a 72 c 175 g 229 t

Query Match 2.5%; Score 70.4; DB 12; Length 795;
Best Local Similarity 44.8%; Pred. No. 0.00044;
Matches 269; Conservative 0; Mismatches 331; Indels 0; Gaps 0;

QY 1852 ggaattggtatatactactgtagatgtagcagcgaacagaacgagcattatatacagctt 1911
DB 193 GATTTAATTCCTTTTATTTTAAACATTCACCTAAAGCTGGAAGAACCTTGATTAATAT 232
QY 1912 aacgtlaaagctgcgaagctgatactaccatgaagctgtgaagcgtcaagaaccaa 1971
DB 253 TATGATGAATTCGATTAGAGAAAGAAATGTAACGGAAGAAATAACGTGCAATACGAA 312
QY 1972 gtgggtaaacgtactgaacatccagtcgtgattatgaatlaaagaagaagctggat 2031
DB 313 GATGATGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAC 372
QY 2032 ggtatcagctcagcgaataattggaatcgttagaagaagtaattggttcataattat 2091
DB 373 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 432
QY 2092 gatgtatcacaagcttcaataatccacacatatccatcagctgtggaagctgattat 2151
DB 433 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 492
QY 2152 ctgcgattggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 2211
DB 493 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 552
QY 2212 ggaagatgaagcgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 2271
DB 553 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 612
QY 2272 gctgtgaatgattctatctctcgaagcgtgtagtgaatgaatgaatgaatgaatga 2331
DB 613 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 672
QY 2332 acgggcaatgataaattgaatcattcgaatgaatgaatgaatgaatgaatgaatga 2391
DB 673 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 732
QY 2392 acccaagaaggttattagttaaacgaatgaatgaatgaatgaatgaatgaatgaatga 2451
DB 733 AAACAAATTCACAAATTCACAAATTCACAAATTCACAAATTCACAAATTCACAAATTC 792

RESULT 13
A2676218/c 823 bp DNA linear GSS 14-DEC-2000
LOCUS ENTKE36TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
DEFINITION ENTKE36TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, DNA sequence.
ACCESSION A2676218
VERSION A2676218.1 GI:11813364
KEYWORDS GSS.
SOURCE Entamoeba histolytica.
ORGANISM Entamoeba histolytica.
Eukaryota; Entamoebidae; Entamoeba.

REFERENCE 1 (bases 1 to 823)
AUTHORS Loftus, B., Van Aken, S., and Fraser, C.

TITLE Determination of clone end sequences from Entamoeba histolytica
HML:IMSS sheared DNA library

JOURNAL Unpublished (2000)
CONTACT: Brendan J Loftus
COMMENT Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjl@louisville.org

Clones are derived from the Entamoeba histolytica HML:IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 17
High quality sequence stop: 810.
Location/Qualifiers
1. 823

FEATURES

source

/organism="Entamoeba histolytica"
/strain="HML:IMSS"
/db_xref="taxon:3759"
/clone_lib="Entamoeba histolytica sheared DNA"
/note="Vector: PHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
light size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999)."

BASE COUNT 228 a 206 c 86 g 303 t

Query Match 2.5%; Score 70.4; DB 12; Length 823;
Best Local Similarity 44.8%; Pred. No. 0.00045;
Matches 269; Conservative 0; Mismatches 331; Indels 0; Gaps 0;

QY 1852 ggaattggtatatactactgtagatgtagcagcgaacagaacgagcattatatacagctt 1911
DB 782 GATTTAATTCCTTTTATTTTAAACATTCACCTAAAGCTGGAAGAACCTTGATTAATAT 723
QY 1912 aacgtlaaagctgcgaagctgatactaccatgaagctgtgaagcgtcaagaaccaa 1971
DB 722 TATGATGAATTCGATTAGAGAAAGAAATGTAACGGAAGAAATAACGTGCAATACGAA 663
QY 1972 gtgggtaaacgtactgaacatccagtcgtgattatgaatlaaagaagaagctggat 2031
DB 662 GATGATGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAC 603
QY 2032 ggtatcagctcagcgaataattggaatcgttagaagaagtaattggttcataattat 2091
DB 602 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
QY 2092 gatgtatcacaagcttcaataatccacacatatccatcagctgtggaagctgattat 2151
DB 542 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
QY 2152 ctgcgattggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 2211
DB 482 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423
QY 2212 ggaagatgaagcgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 2271
DB 422 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 363
QY 2272 gctgtgaatgattctatctcgaagcgtgtagtgaatgaatgaatgaatgaatgaatga 2331
DB 362 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 303
QY 2332 acgggcaatgataaattgaatcattcgaatgaatgaatgaatgaatgaatgaatga 2391
DB 302 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 243

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2002, 07:01:13 : Search time 102 Seconds
(without alignments)
6704.350 Million cell updates/sec

Title: US-09-884-696-1
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Sequence: 1 atgcacataataatgaat.....tttgcctcaagtgttag 2784

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Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/lna/5B_COMB.seq: *
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6: /cgn2_6/ptodata/2/lna/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	815.6	29.3	3311	1	US-07-777-715-6 Sequence 6, Appl1
2	815.6	29.3	3311	1	US-08-170-126-1 Sequence 1, Appl1
3	815.6	29.3	3311	3	US-08-954-418-1 Sequence 1, Appl1
4	814.4	29.3	2794	1	US-07-960-932-1 Sequence 1, Appl1
5	814.4	29.3	2794	1	US-07-908-253-1 Sequence 1, Appl1
6	814.4	29.3	2794	1	US-08-455-970A-1 Sequence 1, Appl1
7	814.4	29.3	2794	1	US-08-387-156-5 Sequence 5, Appl1
8	814.4	29.3	2794	2	US-08-694-865-5 Sequence 5, Appl1
9	814.4	29.3	2794	2	US-08-878-748-5 Sequence 5, Appl1
10	814.4	29.3	2794	2	US-08-535-837-1 Sequence 5, Appl1
11	814.4	29.3	2794	3	US-09-124-491-5 Sequence 5, Appl1
12	814.4	29.3	2794	6	5476657-2 Patent No. 5476657
13	814.4	29.3	2817	1	US-07-960-932-9 Sequence 9, Appl1
14	814.4	29.3	2817	1	US-08-455-970A-11 Sequence 11, Appl1
15	814.4	29.3	2838	1	US-07-960-932-8 Sequence 9, Appl1
16	814.4	29.3	2838	1	US-08-455-970A-9 Sequence 9, Appl1
17	814.4	29.3	2861	1	US-07-960-932-10 Sequence 10, Appl1
18	814.4	29.3	2861	1	US-08-455-970A-13 Sequence 13, Appl1
19	814.4	29.3	2934	1	US-08-387-156-7 Sequence 7, Appl1
20	814.4	29.3	2934	2	US-08-694-865-7 Sequence 7, Appl1
21	814.4	29.3	2934	2	US-08-878-748-7 Sequence 7, Appl1
22	814.4	29.3	2934	3	US-09-124-491-7 Sequence 7, Appl1
23	814.4	29.3	3229	1	US-07-777-715-8 Sequence 8, Appl1
24	814.4	29.3	3229	1	US-08-170-126-3 Sequence 3, Appl1
25	814.4	29.3	3229	3	US-08-954-418-3 Sequence 3, Appl1
26	814.4	29.3	3646	3	US-08-619-812-7 Sequence 7, Appl1
27	800.4	28.8	2802	1	US-08-215-805A-79 Sequence 79, Appl1

28	800.4	28.8	3848	1	US-08-215-805A-1 Sequence 1, Appl1
29	775	27.8	4731	2	US-08-488-706-2 Sequence 2, Appl1
30	775	27.8	4731	3	US-08-772-270A-9 Sequence 9, Appl1
31	636.8	22.9	4190	2	US-08-488-706-3 Sequence 3, Appl1
32	629	22.6	3828	5	PCT-US93-10500-1 Sequence 1, Appl1
33	629	22.6	7721	3	US-08-772-270A-14 Sequence 14, Appl1
34	488.8	17.6	3762	3	US-08-488-706-1 Sequence 1, Appl1
35	485.6	17.4	8370	2	US-08-772-270A-3 Sequence 3, Appl1
36	403	14.5	2278	1	US-08-258-188-1 Sequence 1, Appl1
37	403	14.5	2278	1	US-08-526-813-1 Sequence 1, Appl1
38	403	14.5	2278	5	PCT-US95-08554-1 Sequence 1, Appl1
39	343.2	12.3	2102	2	US-08-694-865-15 Sequence 15, Appl1
40	343.2	12.3	2102	3	US-09-124-491-15 Sequence 15, Appl1
41	341.8	12.3	1635	1	US-08-387-156-9 Sequence 9, Appl1
42	341.8	12.3	1635	2	US-08-694-865-9 Sequence 9, Appl1
43	341.8	12.3	1635	2	US-08-878-748-9 Sequence 9, Appl1
44	341.8	12.3	1635	3	US-09-124-491-9 Sequence 9, Appl1
45	308.2	11.1	6850	4	US-09-298-367B-2 Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-07-777-715-6
; Sequence 6, Application US/0777715
; Patent No. 5273889
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew
; APPLICANT: Campos, Manuel
; APPLICANT: Hughes, Huw P.A.
; TITLE OF INVENTION: CYTOKINE-LEUKOTOXIN GENE FUSIONS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; City: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07777, 715
; FILING DATE: 1991016
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Rodins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 29310-2001320
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3311 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3294
; ;
; US-07-777-715-6
Query Match 29.3%; Score 815.6; DB 1; Length 3311;
Best Local Similarity 60.1%; Pred. No. 1.6e-177;
Matches 1544; Conservative 0; Mismatches 964; Indels 60; Gaps 9;

OY 39 aggcgttaattcaacaagaftctgattaaatacttacttgcgtatcccaagat-- 96
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OY 97 ----tatgatccgcaaaaaggttggactttaatgatatcttatiaaagctgtatgaat 152
Db 591 CCATATGATATCTGACACAGGTATGGTTTACAGATTATAGTCAAGCGCGCAAGAGT 650
OY 153 aggtatgtctgtttagcagaagaagcctaatcaacccgaaacgcaaaaatctgttga 212
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OY 213 cagcgttaaatcagttctctctcccaacaacgtgatctctatcttcgtcaaaaaat 272
Db 711 CACGATTCAAAACCGCTATTGGCTTAACCTGAGCGCTGGCATTTGTATCCGCTCCACAAAT 770
OY 273 agaaaagttcttcaaaaaacattctaccaataagltagccaaaggttgaacagltaga 332
Db 771 TGATTAATTTGCTACGAGAA-----ACTAAAGCAGGCCAAGCAATTAGGTTCTGCCGA 821
OY 333 aaatatgtatcgttaaataggttaagcaagaatgatatctcaaatgaagctctctttt 392
Db 822 AAGCATTTGTACAAATGCAAAATGCAAAAGCCAAAGCTGATTATCTGCAATTCATATTT 881
OY 393 gggcactgtcatagcgggtatagaactgtatctttaaacaanaaaggtgatgtgaac 452
Db 882 AGGCTCATGATTGGCTGGAATGGATTATGAGGCGCTTACAGAA---TAACAGCAACCA 938
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OY 513 ggaatctcaaaaagattgtagcaattcttctcaagttagaagttatctatctatctc 572
Db 999 TTCACATAAAACACTTGAAGAAATTTGGTGAGCAATTTAGTCAATTTGGTTCAAAACCTCA 1058
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Db 1119 ACCTGGCTTGGTTAGATGATTATCTCAGGCTATTTATGGGCGCAACAGCTGCACTTGT 1178
OY 690 tttagcgagataaaaatgtagcactgcgcgcaaaaagttgcgtcaggttttgaatlaagca 749
Db 1179 ACTTGACGATTAATAATGCTTCAACAGCTTAATAAGTGGGTGGGTTTGAATTTGGCAAA 1238
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OY 810 tgcgtgtctatacaactacgt 869
Db 1299 AGCAGGTTATCTTCAACGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1358
OY 870 aattagttccttgcgtatgaatgtcaagcagataaatacaatcatgctgaatgtcttga 929
Db 1359 GATTACCCATTGATTTGGCGGTATTTGCCGTAATTTAATTCANCGAAAAAGTTTGA 1418
OY 930 tgaagtttgcacaaacaaatccgaaatcttgcgtatgtgtgtgtgtgtgtgtgtgtgtgt 989
Db 1419 GATTTATGCGCAACGCTTAAAAAATTTAGCTATGACGAGATTAATTTATGACAAATA 1478
OY 990 tcaaggt 1049
Db 1479 TCAGCGGGGACACAGGAGCTATTTGATGCAATGGTTACTGCAATTAATACCGCAATGGCGCG 1538
OY 1050 agttctgtcgt 1109
Db 1539 TATTTGCTGGT 1598

OY 1110 attagttcaggtgtgtacaggaattgactctcggaaatttagaagcgtctaaacggcaat 1169
Db 1599 ATTAGTATCTGGGATTAACCGGTGTGATTTCTAGATTTCTGCAATTTCTTAAACAGCAAT 1658
OY 1170 gtttgaaggt 1229
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OY 1230 cgttcgaactaatttgaataaagctatgtatctcgtttagtctgtctatttagctaataa 1289
Db 1719 CGGTAGAACTACTTTGAAATGTGTACGATGCCCTGTATCTTGGCAATTTTCAAGATA 1778
OY 1290 cttaaaatttctcgtgtcgttaataaaggttgaagcgtgtgaaggtgtgtgtgtgtgtgt 1349
Db 1779 TATGAATTTCTTACTGAACTTAACAAAGATTACAGGCAAGAGCTGTATGCTGCTTTAC 1838
OY 1350 ccaacaagcgttggataataataattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1409
Db 1839 TCAGCAGCAATGGGATTAACCAATTTGATTTAGCTGTGTATGACCGTTTAGTGAAAA 1898
OY 1410 cattaaagcgggaagaagcttagcagaatgcttltgaagatgcaagaagaatgtgaagctgt 1469
Db 1899 AGTCTTAGTGTGTAAGCCATGTGATGGCTTTGAAAGAGGCAACACATTAATAAGCCGA 1958
OY 1470 ttcaataataactttgtagtgaataaagctgtatcatagacattagttatcaaatgtgga 1529
Db 1959 TAATTAATGTAAGTGTGATTTGGCAACGCTATTTATTTGATGATGATTAATTCGGGTAAAC 2018
OY 1530 aaaaacgcaagcgttgcattctacttcgtgttgaacagcagaagcgtgaatcagctga 1589
Db 2019 GAATTAATGTAAGTGTGATTTGAAAGCCATGTGATTTAGCCCGGGAAGAGCATGTGA 2078
OY 1590 aagtttaactaatgttaataactcttatataatgaagttaaatlttgcgcgtgttaaanaa 1649
Db 2079 ACGGTCAAAACAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2138
OY 1650 ctgcaagttacagatgtagaagcgttagtcttaataatgaattcttcaaatlttaagcgt 1709
Db 2139 CTGGAATAATTAACAGATGTGTGACAGCAATTTCTACTTTGATTTAATTAATTAATTAAT 2198
OY 1710 tgtacggagacagaagcagaagcagagattgtgtctaatgttaatgtgaagaa----- 1761
Db 2199 TATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2258
OY 1762 -----gtgtgcaatgtgcatacttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1808
Db 2259 TGCCAAACTTGTGAAGGTGATGACAAACGTAATTTGTTGTTCTGTGTAACGCAAAATTTGA 2318
OY 1809 tgtgtgagatgtgacacagatcgtgtctctatagtaagaagcggagattgtgtaatatctac 1868
Db 2319 TGGCGGTGAAGGTATACAGACGAGTTCACTATAG---CCGTGGAATACTATGTGTGCTTAAAC 2375
OY 1869 tgtagatgttagcaggttgaacagaagaagcaggtatatacagttaatctgtgaagttgtcgt 1928
Db 2376 TATTGATGCAACCAAGAGACCGAGCAAGGTAGTTAATCCCTAATATGCTTTGTGAAC 2435
OY 1929 aggtgtatcttcaatgaagttgtgaagcgttcaagaagaacaaaggttgggttaaacgttactga 1988
Db 2436 CGGTAAACCTACACGAGAGTGACTTCAACCCATTAACCGCATTAATTTGGCAACCGTGAGGA 2495
OY 1989 aactatccagatcgtgtatltgaatlaagaagaagtttggatagttatcaagttactacga 2048
Db 2496 AAAATATGATATATCGTATAGCAATTAACCAACACCAATG---CCGTTATTTACACCAAGA 2552
OY 2049 taatttgaatcagtagaagaagatgt 2108
Db 2553 TACTTTGAAGCTGTGTGAAGAAATTTATGATCATCAATTAACGATTAATTTTAAAGGTAG 2612
OY 2109 taaattcaacgacatattccatagttgtgtgaaggtgtatatttactcgaatgtgtgtgtgtgt 2168
Db 2613 TAACTTCAATGATGCTTTAAACGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2672
OY 2169 tgaacacgctgt 2228

Db 2673 CAATGACCGCTTATTGGTGTAAAGCGATGATATTCTGAGTGGTGAATGGTATGA 2732
Qy 2229 tttaactgcatgagcgtctcgtgtgtagtgcataaagtgtgtgtgtgtagtgcata 2288
Db 2733 TTTTATGAGGCGGTAAAGCGAACCTATTACACGGTGGCAAGGCGATGATATTTT 2792
Qy 2289 tactcttcggaagagtgatgtagtacttctgtacgtagcgcgagcagatgaatc 2348
Db 2793 CGTTCACCGTAAAGCGATGATGATATTATTTACCGATTTGACGCGAATGATTAAT 2852
Qy 2349 agcatctgcagatgcacaataatcgtatcatatgatgtgaacgctacccaagaggtatcat 2408
Db 2853 ATCATTTCTGATTCGAACTTAAAGATTAACTTTGAAAGTTAAACA---TATCT 2909
Qy 2409 agttaaagcaatgataatcagtgtagtataacataccaagatgtagatcaatacaaa 2468
Db 2910 TGTATCAGCAATAGCAAAAGAGAAAGTACCATTCAAAACTGTTCCGAGAGGCTGA 2969
Qy 2469 tttaacaaa-----ttatcaagtaataaagacagatcataaattgaagcaactat 2519
Db 2970 TTTTGTCTAAAGAACTGGCTTATTATTAAGCACTAAAGATGAGAAAATCGAAGAAATCAT 3029
Qy 2520 tggtaagatgtagtataatcacttcgcagatccaatgtataaatttt 2567
Db 3030 CGGTCAAAATGGCGAGCGATCACCTCAAGCAAGTGTGATGATCTTAT 3077

RESULT 2
US-08-170-126-1
; Sequence 1, Application US/08170126
; Patent No. 5594107
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW
; APPLICANT: CAMPOS, MANUEL
; APPLICANT: HUGHES, HUM P.A.
; TITLE OF INVENTION: CYTOKINE-CYTOTOXIN GENE FUSIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,126
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/777,715
; APPLICATION DATA: US 07/571,301
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9000-0013.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

FEATURE:
NAME/KEY: CDS
LOCATION: 1..3294
US-08-170-126-1
Query Match 29.3%; Score 815.6; DB 1; Length 3311;
Best Local Similarity 60.1%; Pred. No. 1.6e-177;
Matches 1544; Conservative 0; Mismatches 964; Indels 60; Gaps 9;
Qy 39 aggccttgaatccaagaagtcgtgattaaataaacttacttctgtgctatcccaagaat-- 96
Db 531 AGCGCGCAGTTCTTTAAAACTGGGCGCAAAAAATTTATCTTATATTCGCCAAATTA 590
Qy 97 -----tatgatccgcaaaaaggttggactttaaataatgtatttaagaagctctgtatga 152
Db 591 CCAATATGATATACGTGCAACAGGTAAAGTTTACAGATTTTATGTCMAACGCCCGCAAGATT 650
Qy 153 aggtatgtccgttttagcagaagaagcctaatacacaactgaaacagcaaaaatctgttga 212
Db 651 GGGCATTTGAGGTACAAAGAGAGAGAACCAATATATTGCAACAGCTCAAAACAGTTTACG 710
Qy 213 cacagtaaatcgaagttctctctctcacaacaactgtagtctatcttcgtcaacaaat 272
Db 711 CACGATTCAAACCGCTATTGGCTTAAGTGAAGCGGATGTTGTTATCCGCTCACAAAT 770
Qy 273 agaaagttcttacaataaacatctaccaataagttgccaagaaggttagaagttaga 332
Db 771 TGATTAATTTGCTACAGAAA-----ACTTAAAGCAGGCCAACATTAAGTTTGGCGGA 821
Qy 333 aaatctgacgcgaatcttgaagcaagtaagtaataatcaacatcaagctctcttt 392
Db 822 AAGCATTTGTACAAATATCAATTAAGCCAAACTGTTATTTCTGGCATTCATTTATTTT 881
Qy 393 gggcactgcattagcgggtatagaacttgatcttcaatacaaaaaggttgaagtcgacc 452
Db 882 AGGCTAGTATGTCGTGAATGATGATTTAGTAGAGCGCTTACAGAA---TAAACAGACACA 938
Qy 453 tgaagcttggcttaagaactgtagtacttgatataagagataatgtatcatctatc 512
Db 939 ACATGCTCTTGTCTAAAGCTGGCTTGAAGCTAAACAAATTCATTAATTAATTAATTTGCTAA 998
Qy 513 gagtactcaacagatctgaagcattctctcgaagttgaagaagttgctactatc 572
Db 999 TTCAGTAAAAACACTTACGCAATTTGGTGAACCAATTAATTAATTTGTTCAAAACCTTACA 1058
Qy 573 gcaagctaaagcttctctcctaataagaaacaggtgcacaaacttaaat---tttctaa 629
Db 1059 AAATATCAAAAGCGTTAGGACTTTAGGAGACAAACTCAAAAATATTCGTGACATTGATTA 1118
Qy 630 aacaaactcgtgttggaaataataactgtagtctcactcaggcaatcttcgagcttgc 689
Db 1119 AGCTGGCTTGTGTTAATGATGATCTCAAGGCTATTTATCGGCGCAACAGCTGCATCTGT 1178
Qy 690 tttagcgataaaaatgcatcgactggcaaaaaggttgcgcaggttttgatgaagcaa 749
Db 1179 ACTTGCAGATTAATAATGCTTACACAGCTAAAAAAGTGGGCTTTTGATTTGGCAAA 1228
Qy 750 tcaagttatgtagtaatgtaacaaagaacttctcatalgttttagacaaagtgctgc 809
Db 1239 CCAAGTTGTTGTAATTAATTAACCAAGCGTTTCTTTACATTTTACCCCAAGCTGTTGC 1288
Qy 810 tgcgtgctatcaactcgt 869
Db 1299 AGCAGGTTTATCTTCACTGGGCTGTGGCTGCTTATATGCTTCTCTCTCTCTCTCTCT 1358
Qy 870 aattagtccttggcatttgaatgaagcaagaataatcaacatgctgaatgctgtcga 929
Db 1359 GATTAGCCCATTTAGCATTTGCGGATTTGCGGATTTTAAATTAATCAATCAAAAAAGTTTGA 1418
Qy 930 tgaatttgcacaaacaaatccgaaatattggtatgtagtgggagatcatattatgtcgaata 989
Db 1419 GAGTTATGCGCAAGCTTTAAATAATTAAGCTATGACGAGATTAATTAATTAAGCAGATA 1478

QY 1929 aggtatatactaccatgaagtttgaagcgtlcaagaacccaagtggttaagctactga 1988
DB 2436 CGGTAAAGCACTACACAGACTTCAACCCGATTAAGTGGGCAACCGTGAGAGA 2495
QY 1989 aacatccagatcgttattatgaatcaagaagaagttggtatgtatcaagtcacga 2048
DB 2496 AAAAATGANTATGCTATAGCAATTAACCGACCATG---CCGGTTATTAACCAAGA 2552
QY 2049 taattgaatcagtagaagaagtaattggttctcaatttaataatgatatcaaggttc 2108
DB 2553 TACCTGAAGAGCTGTGAAGAAATTAACGATACATACATATCTTTAAAGGTAG 2612
QY 2109 taattgaagacatctccatagtgtagaagtgatgaattactgaatgtagtgcgag 2168
DB 2613 TAACTTCAATATGCTTTAAGGAGTGTGATGATGATCTTTGACGTTAAGGACGAG 2672
QY 2169 tgaagacgcgttctgtgtgtagaaggaacgacatcttctgtagatgaagagcagatga 2228
DB 2673 CAATGACCGCTTATTTGGTGTGAAGCGATGATTTCTCGATGTGGAAATGATGATGA 2732
QY 2229 ttactcagatgaggttctgtgtgatgatatgaatggtgtgtgtgtgtgtgtgtgtgt 2288
DB 2733 TTTATATCATGCGGTAAAGGCAACGACCTATTACAGGTGGCAAGGCGATGATATT 2792
QY 2289 tatcttcggaaggtgtagtgaatgatacttctgacgagtgcaagcgcaatgaataat 2348
DB 2793 CGTTCACCGTAAAGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 2852
QY 2349 agcatltagcagatgaataatactatgatataatgaatgaacgtacaaagaggtatgat 2408
DB 2853 ATCATTTCTCTGATTCGAATTAAGATTTAATTAAGATTTAAGATTTAAGATTTAAG 2909
QY 2409 agttaagaagaatgatcttcagtagatgaataacatgaagatgtagatgaataacaa 2468
DB 2910 TGTCTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2969
QY 2469 tttaacaa-----ttatcaagaataaacaacatgaataaattgagcaactaat 2519
DB 2970 TTTTGTCTAAAGAGTCCCTAATTTAAGCAACTTAAGATGAGAAATGCAAGAAATCAT 3029
QY 2520 tggtaagaatgtagtatatcatcacttcgcagatcaaatgataaattt 2567
DB 3030 CGGTCAAAATGCGAGCGGATCCTCAAGCAAGTTGATGATCTTAT 3077

RESULT 4
US-07-960-932-1
Sequence 1, Application US/07960932
Patent No. 5422110
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HOW P. A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
TITLE OF INVENTION: CHIMERAS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/960,932
FILING DATE: 19921014
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0016, 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2794 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2778
US-07-960-932-1

Query Match 29.3%; Score 814.4; DB 1; Length 2794;
Best Local Similarity 60.2%; Pred. No. 2.9e-177;
Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

QY 53 caaagctcgatgaataaatacttacttgctatcccaagat-----tatgacgcg 106
DB 29 CAAAACTCGGGGCAAAAAAATTTCTCTATATTTCCCAAAATTTACCAATATGATCTG 88
QY 107 aaaaagctggagctttaaagatatttaaaagctgctgataatgtagatgctgt 166
DB 89 AACAAAGTAAATGTTTACAGATTTAGTCAAAAGCGCGGAAGATTTGGGATTTAGGTAC 148
QY 167 tagcagaagagcctaatacactgcaaacgcaaaaaaactcgttgacacaglaaact 226
DB 149 AAAGAGAAAGACGCAATTAATTTGCAACAGCTCAAAACAGTTTGGCAGCATTTAAACG 208
QY 227 ttctctctcaacaacactgtagtattcttctgcaaaaatgtgaagttctac 286
DB 209 CTATTGGCTTACGTGAGCGCTTGTGTTATCCGCTCCCAAAATTTGATTAATTTGCTAC 268
QY 287 aaaaacattcacaataagttagcacaaggttagacagtgtagaataatgatcgtga 346
DB 269 AGAA-----ACTTAAGCAGCGCCAGCATTTAGTTTGGCGAAAGCATTTGTACAA 319
QY 347 aattagtagaagcaagtaatgatatacaacataaagctcttcttgggcaatgtag 406
DB 320 ATGCAATTAAGCCAAACTGATTTATCTGCAATTCATTTTATGAGCTGATTTGG 379
QY 407 cggatagaaactgaattccttaacaaaagaagtgatgcgcacccatgacttgctga 466
DB 380 CTGGAATGATTTTATGATAGAGCCTTTACGAA---TAACAGCAACCAACATGCTCTTGCTA 436
QY 467 aagctagatgacttgatgaatgaataatgtaataatctcgaagatcgaacga 526
DB 437 AAGCTGGCTTGAGAGCTTACCAATTCATTAATGAATAATTTGCTAATTCAGTAAACAC 496
QY 527 ttgaagcatttctcacaagttagaagttagttctacatatacgaagctgaagct 586
DB 497 TTGACGAATTTGGTGAAGCAATTTACTCAATTTGGTTCAAACTACAAAATATCAAGCT 556
QY 587 tctcctaataagaacaagttgcaaaacttaaat---tttcttaaaaacaaatcttgct 643
DB 557 TAGGACCTTTAGAGACCAACCAAAATTTGAGTGAAGCTGATTAACCTGGCTTGCTT 616
QY 644 tggaaataatcagttggtctatcgaagcattctgcaggtcttgctttagcagataaa 703
DB 617 TAGATGTTATCTCAGAGGCTATTATCGGCGCAACAGCTGATCTTGTAGATTAATA 676
QY 704 atgcatacagctgcaaaaaagttgctgcaagtttgaatgaacataaagttatgtagta 763
DB 677 ATGCTTCAACAGCTAAAAAAGTGGGTGGCTTTGGAATTTGGCAACCAAGTTGTTGGTA 736
QY 764 atgtaacaaagcaatttctcatalatgttttagcaaacagttgtgtgtgtctatcaa 823

D	b	1757	AAGGTGATGCACACGATTATTGGTTCTCGTACACGCCGAATAATGTATGGCGTGAAAGTT	1816
O	y	1823	acgatcgctcctctatagtaagaacgaggatcttggtataatactacgctagtcgcga	1882
D	b	1817	ACGACCGCAGTTCACTATTAC---CCGTGGAAACTATAGTCCTTTAACAATTACGACCA	1873
O	y	1883	gtgcacaagaagaaggcaattacagttaaactcgtaaagtctgcctgaqgtatalcc	1942
D	b	1874	AAGGACCAGCGCAAGGTAGTTATACGGTAAATCGTTTCGTAAACCCGGTAAAGCATAC	1933
O	y	1943	atgaagcttgygaacgcctcaagaaccgaagctgggtaaaccgtactcaactccagtatc	2002
D	b	1934	ACGAAGGACTTCAACCCATTACCGCAATTGTGTGGCACACCGTAAGAAAAAATAGATATC	1993
O	y	2003	gtgattaatgaattaaagaagaagtctggtagtcatcagtlcataccgataatttgaalcac	2062
D	b	1994	GTCATGACAAATACCGACGCCATG---CCGGTTATTACACCAAAGATACCTTGAAGGTG	2050
O	y	2063	tagaagaagtaatttgttctccaatttaagatgatatcaaaggtctctaattcaacgaca	2122
D	b	2051	TTCGAAGAATATTCGGTATCATCAATAAACGAATCTTTAAAGTAGTAAGTCAATGATG	2110
O	y	2123	tattccaatgctggagaagtgatattactcgaatggctgctgctgtyaacgccctgt	2182
D	b	2111	CCTTTACGSGTGTGATGCTGCTGATACATATTGACGGTACAGCGCAATGACCGCTTAT	2170
O	y	2183	ttggctgtaagaagcaacgacatcgactctctcgagatgaagcgaatgatattactcgatgcg	2242
D	b	2171	TTGGTGGTAAAGSCGATGATATTCTCGATGGTGGAATGGTATGATTTTATCGATGGCG	2230
O	y	2243	gttcctgctgatctgctatcaaatgctgtgcctgctgaatgagctcatctcttggaaag	2302
D	b	2231	GTTAAGGCCAACGACCTATTACACGGTGGCMAAGGCGATGATATTTTCCTTACCGTTAAG	2290
O	y	2303	gtgatgtaatgaatctcttgtaacgatgagcagcggaatgaataattagcatcttgcagatg	2362
D	b	2291	GCGATGCTAATGATATTATTATACCGATCTGACGGCAATGATTAATTAATCATCTCTGATT	2350
O	y	2363	caaatatctcgaatattatgatgtgaacgctacccaagaaggtatlaagttaacgaaatg	2422
D	b	2351	CGAACTTAAAGATTTAAACATTTGAAAAGTTAAACA---TAATCTGTCAACAGATA	2407
O	y	2423	atcaatcaggtagttatcaatacacaagaatggttacatacatcaattcaaaaa-----	2477
D	b	2408	GCAAAAAGGAAGGACCATTTCAAAACCTGCTCCGAGAGCCTAATTTTCTTAAGAG	2467
O	y	2478	----tatacaagtaataaacaacgatacaaaaattgagcaactaattgtaagaatgta	2533
D	b	2468	TGCTTAATTTAANAAGCACTAAAGATGACAAATAATGACAGAAATCATCGCTCAAAATGGCG	2527
O	y	2534	gtatatacatcttcgaatcaaatlgataaaatttt	2567
D	b	2528	AGCGGATCACCTCAAGCAAGTTGATGATCTTAT	2561
 RESULT 6 US-08-455-970A-1 Sequence 1, Application US/08455970A Patent No. 5708155 GENERAL INFORMATION: APPLICANT: POTTER, ANDREW A. APPLICANT: REDMOND, MARK J. APPLICANT: HUGHES, HOW P.A. TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN TITLE OF INVENTION: CHIMERS NUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS: ADDRESSEE: REED & ROBINS STREET: 285 HAMILTON AVENUE, SUITE 200 CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA ZIP: 94301				

Query	53	29.3%	Score 814.4	DB 1	Length 2794
Best Local Similarity	60.2%	Pred. No. 2.9e-177			
Matches 1538	Conservative 0	Mismatches 956	Indels 60	Gaps	
<p>COMPUTE: READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patentin Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/455,970A</p> <p>FILING DATE: 31-May-1995</p> <p>CLASSIFICATION: 424</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US 07/960,932</p> <p>FILING DATE: 14-OCT-1992</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: ROBINS, ROBERTA L.</p> <p>REGISTRATION NUMBER: 33,208</p> <p>REFERENCE/DOCKET NUMBER: 9001-0016.10</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: (415) 327-3400</p> <p>TELEFAX: (415) 327-3231</p> <p>INFORMATION FOR SEQ ID NO: 1:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 2794 base pairs</p> <p>TYPE: nucleic acid</p> <p>STRANDEDNESS: double</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: DNA (genomic)</p> <p>FEATURE:</p> <p>NAME/KEY: CDS</p> <p>LOCATION: 1..2778</p> <p>US-08-455-970A-1</p>					
Query Match	29.3%	Score 814.4	DB 1	Length 2794	
Best Local Similarity	60.2%	Pred. No. 2.9e-177			
Matches 1538	Conservative 0	Mismatches 956	Indels 60	Gaps	
Query	53	caaaagtctgatatataaaactcttaacttgcgtatcccaagaat-----tatgatccgc	106		
Db	29	CAAAAGCTGGGGGCAAAAATAATTATCCCTCTATTATCCCAAAATTCACCAATGTGATACG	88		
Query	107	aaaagaagtggaacttaaaagtatttataaagctgcgtgataatgaattatgctgcgt	166		
Db	89	AACAAGGTAATGGTTTACAGCAATTTAGTCAAGCCGCGGACAGATTGGGAGATTGAGTAC	148		
Query	167	tagcagaagagcctcaactcacactgaacagcagcaaaaaactctgttcaacagtaaaatcagt	226		
Db	149	AAAGAGAAGAACGCGCATATATATTGCAACAGCTCAACAGCAACAGATTAGCAGCATCAACCG	208		
Query	227	ttctctctctacacaaactggtatctgctatcttctgcacaaatlagaaaaagctcttac	286		
Db	209	CTATTGGCTTAACTGAGCGTGGCATTTGTTATCCGCTCCACAAATTTGTAATTTGCTTAC	268		
Query	287	aaaacactctcaacaaatgaatgtagcgaaggttagagacagtgtagaaaaatattgtagcga	346		
Db	269	AGAAA-----ACTTAAGCAGGCGCAAGCATTTAGTTCTGCCAAGACATTTGACAA	319		
Query	347	aattaggtlaaagcaagtaatttatatacaacatlaagctcttcttttggcgaactgcatlag	406		
Db	320	ATGCAATTAAGCCCAAACTGTATTATCTGGCATTCATCATTTTATTTAGGCTCAGATTTAGG	379		
Query	407	cggatataagaacttgatctctttaaacaacaaagtgatgctgcacactgtagcttggcta	466		
Db	380	CTGGAATGAGATTGTAGATGAGCCCTTACGAA---TAAACAGCAACCAACATGCTCTTGGTA	436		
Query	467	aagctagtagtacttgatgtaataagataaattggtgaactctatcttaagtgtaactcaaaaga	526		
Db	437	AAGCTGGCTTGGACTTAACAATTCATTAATTTGAAAAATTTGCTAATTCAGTAAACAC	496		
Query	527	ttgaagaacttcttcccaagcttagcaaaagcttaggtctctacacatctcgcagagctaaaggct	586		
Db	497	TTTGACGAATTTGGTGAGCAATTTAGTCAATTTTGGTTCAAACTACAAATATACAAAGGCT	556		
Query	587	tctctaatatagaacaaagcttgcacaaacttaaat--tttcttaaaaaaactcttgglt	643		

Db 557 TAGGACATTTAGAGACAACTCAAAAATATCGGTGACATTGATTAACCTGGCTTGCTT 616
 Oy 644 tggaaatattacttggttgctatcagcattcttcgagcttcttgcttgagcgtataaa 703
 Db 617 TAGATGTTATCTCAGGGCTATTATTCGGCGCAACAGCTGCACCTTGCTTACTTGACATTA 676
 Oy 704 atgactcgtctgcagaaaaagttgctgcaggttttgaaatgaacatcaattatgtgta 763
 Db 677 ATGCTTCAACAGCTAAAAAGGTGGGTGGGGTTGAAATGGCAACCAAGTTGGTGA 736
 Oy 764 atgtaacaaaagcaattcttcataatgttttaagcaaacgtgttgctgtctgtctataa 823
 Db 737 ATATTACCAAGCCGTTCTCTTACATTTAGCCCAACGGTTGACACAGGTTTATCTT 796
 Oy 824 ctactgctgctgtctgtcttacttaactcaatcgtatgttgcaattagtccttctg 883
 Db 797 CAACGGGCGCTGTGGCTCTTTAATGCTTCTACTGTTCTCTTGCGATTAGCCCATTA 856
 Oy 884 cattatgaatgcagcagataaattcaatcactgctactgcttcttgatgagtttgcaaac 943
 Db 857 CATTTGGCGGTATTCGCATTAATTATTCAGCAAAAAGTTTAGAGATTATGCGCAAC 916
 Oy 944 aattccgaaaatttggcctatgatggtggtatcattatgtgcgtgaatatacagcgtgtg 1003
 Db 917 GCTTTAAAAAATTAGGCTATGACGAGATTAATTATTCAGCAAAATATGACGGGGAACAG 976
 Oy 1004 gtactatgaagcttacttaactcaatcactgaagcagcattagtgctgcttctgtgtg 1063
 Db 977 GGACATTATGATGCATCGGTTACTGCAATTAATACCGCATGTGCCCTATGCTGGTG 1036
 Oy 1064 ttccgcgtcgtcgtgtagatcgtctgtgtgbcacgcatgacatgagtttgcaagtg 1123
 Db 1037 TGTCGCGCTGCACACCGCGCTGGTTATGCTTACCCATTGCCATTGATGATCTGGGA 1096
 Oy 1124 ttacaggttgatctctcgtgaatttgaagcgtctcaacagcgaattgttgaagtgtg 1183
 Db 1097 TTACCGGTATTAATTTCTCGATTCGCAATTTCTTAACCAACCAAGTTTGACACGTTG 1156
 Oy 1184 ctacacgttcaagaagtaaaattttagagtggtgaaagcaaaattgcggtcagaactat 1243
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 Oy 1244 ttgataaagcgtatgactcgttactgctgttactttagcctaactaaatttctgt 1303
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 Oy 1304 ctgagctaaataaagaagttggaagcgtgaagcgttattgcaatcccaacaagttgg 1363
 Db 1277 TGAACCTTAACAAAGAGTTTACGSCAGAACGTCATCGCTATTACTCAGCAGCAATGGG 1336
 Oy 1364 ataatcaatatttgtagttagcaggtattaccaaatltgggtgaacgcatlaagacgtgaa 1423
 Db 1337 ATAAACAACATTGCGATTATAGTGTGATTTAGCCGTTTAGGTGAATAAGCTTAACTGGA 1396
 Oy 1424 aagcttatcgcagatgcttttgaagaatggcaagaagaattggaagcgtgttccaatlactt 1483
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 Oy 1484 tggatgctaaaactgtgtcactagacatttagaattcaaatgaggaaaaaaagaagaagct 1543
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 Oy 1604 gtaaatcacttatataataaagttaaatcgcagcgtgttaaaaaactgtgcaagttacag 1663
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Db 1637 ATGTGACGAAGTTCTACCTTTGATTTAACTAACGTTGTCACCGATTGATGAT 1696
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 Db 1697 TAGCAATGCTGGAATTTACTTAACCAAGAAACCAAAAATTAATTCGCAACTGTGTG 1756
 Oy 1763 ctggcaatgacgatatcttgttggtcaaggttaaaatgaataatcgtatgagtgagac 1822
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 Oy 1823 aagatcgtctctctatagtaagaagagattgtgtaataatcgtatgagtgagta 1882
 Db 1817 ACGACCGAGTTCTACTATAG---CCGTGGAACCTATGAGTCTTTAACTATGATGACCA 1873
 Oy 1883 gtcacacagaagcagcagcttataacgtataatcgttaaggtgtgctcagagttatctacc 1942
 Db 1874 AAGAACCGGAGAGGTATGATTATACCGTAATTCGTTGCTGTAAGAAACCGTAAAGCATAC 1933
 Oy 1943 atgaagttgtgaagcgtlcaagaacaaagttggttgaacgactaagtaactccagatc 2002
 Db 1934 ACGAAGTGAATTCACCCCATCCGATTCAGTGTGGCGCAACCGTGAAAGAAAATAGAAATTC 1993
 Oy 2003 gtgattatgaattaaagaagttgtgtatggttatcagttcactacagataattgaaatcag 2062
 Db 1994 GTCATGCAATTAACCGACCAATG---CCGTTATTTACCAACCAAGATACCTTGAAAGCTG 2050
 Oy 2063 tagaagaagtaattgtgtctcaattlaaagtatgtaattcaaaagttcctaattcaacagaca 2122
 Db 2051 TTGAAGAATTTATCGGTACATACATACATATCTTTAAAGGTATGTAAGTTCAATGATG 2110
 Oy 2123 tatccaatgtgtgtgaaggtatgattactacogattgtgtgtgtgtgtgtgtgtgtgtgtgt 2182
 Db 2111 CCTTTAACGGGCTGATGATGCTGATTAATTTAGACGGTAACGACGCAATGACCGCTTAT 2170
 Oy 2183 ttggtgttaaagcagacatcgtacttctgtgagatgaaagcagattactacgtatgctg 2242
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 Oy 2243 gtctcgtgatgatgtatlaaattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2302
 Db 2231 GTAAAGCAACGACCTATTATACGCTGCGCAAGGCGGATGATTTTCTGTCACCGTAAG 2290
 Oy 2303 gtgatgttaagtatactcttgaacgtgcaagcaggaatgaataatgaacatttgagtgagtg 2362
 Db 2291 GCGATGGAATGATATTTTACCGATTTCTGACGGAATGAATTAATTAATCAATTCCTGTGAT 2350
 Oy 2363 caaatatcgtatattatgattgaagcgtaccaaagaggtatattagttaaagcaaatg 2422
 Db 2351 CGAATTTAAAGATTTTAACATTTGAAAAAGTTAAACA---TATCTGTGATCAGCAATA 2407
 Oy 2423 atcattcaggtagttatlaacatlaacaaagattgtatataacatlaacaaatttacaana----- 2477
 Db 2408 GCAAAAAAGAGAAAGTGAACATTTCAAACTGTTCCGAGAGCTGATTTTGGTAAAGAAG 2467
 Oy 2478 ----ttatcaaaagtataaacaagatcataaataatgagcaactaatttgtaaaagtgta 2533
 Db 2468 TGCCATAATTAATAACCACTAAAGATGAGAAATGAGAAATCAATCGTCAAAATGCGCG 2527
 Oy 2534 gtatatcaacttcgatacaaatgttaaaattt 2567
 Db 2528 AGCGATCACCTCAAGCAAGTGTGATCTTAT 2561

RESULT 7
 US-08-387-156-5
 ; Sequence 5, Application us/08387156
 ; Patent No. 5723129
 ; GENERAL INFORMATION:
 ; APPLICANT: POTTER, ANDREW A.
 ; APPLICANT: REDMOND, MARK J.
 ; APPLICANT: HUGHES, HOW P. A.
 ; TITLE OF INVENTION: GDRH-LEUKOTOXIN CHIMERAS
 ; NUMBER OF SEQUENCES: 28


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RESULT      8
US-08-694-865-5
Sequence 5, Application US/08694865
Patent No. 5837268
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNIS, JOHN G.
TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSES:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694, 865
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, Thomas P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
TELEFAX: (415)327-3331
INFORMATION FOR SEQ ID NO.: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2794 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2778
US-08-694-865-5

Query Match          29.3%; Score 814.4; DB 2: Length 2794;
Best Local Similarity 60.2%; Pred. No. 2.9e-177;
Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9

QY   53 caaaagctgataaaaatccttacttggtgcattcccaaga-----tatgatccgc 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   29 CAAAAACTGGGCAAAAATTTATCTCTATTTCCCAAATTCACAAATGATGATCG 88

QY   107 aaaaaagtggaccttaaalgaattatatlaaagctgcatgaattagttatgctcggt 166
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DB   89 AACAAAGTATGGTTTACAGGATTTAGTCAAACGCCGCGAAGGTGGGGATTGAGGTAC 148

QY   167 tagcagaagaagcctaaccacactggaacgcgcaaaaaaatctgctgtgcacaagtaaacgt 226
     ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   149 AAAGAAGAAACCACAATATATTGCAACAGCTCAACAGATTAGCGACGATTCANAACG 208

QY   227 ttcctctctcacacaacacacacacacacacacacacacacacacacacacacacacacacacac 286
     ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   209 CTATTGGCTTAAGTGACCGTGGCATTTGTATTATCCGCTCCACAAATTTGAATAATGTGTAC 268

QY   287 aaaacatcttacaaatagtagccaagaaggtagacaglytagaanaatatgatcgtga 346
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DB   269 AGAAA-----ACTAAAGCAGGCCAAGCATTAGGTCTGCCGAAGACATGTGTACAA 319

QY   347 aattagtgtaaagcaagtaatgatatcaacaattaagctcttttttgggcacgtgcattag 406
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DB   320 ATCCAATATAAGCCAAACACTGTTATTATTCGCGATTCATCAATCATATTATTATTAGGCTCAGATATGG 379

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QY	407	cgggtatagagacttgatcttcttaatccaataaagtgatgctgcacgtatgcttgccta	466
Db	380	CTGGAAATGGATTATAGATGAGGCGCTTACAA--TAAACGCAACCAACAAATCTTGGCTA	436
OY	467	aagctagtatcttgacttgatataagagataatgtgtaatcctatctcagaagtactcaaaaga	526
Db	437	AAGCTGGCTTGGAGCTACAAATTCATTATATGAAATATTTGCTAATTCAGTAAANAAC	496
OY	527	ctgaagcatttcttcacagcttagcaagcttgagttctactaaccgcgtcaaaagct	586
Db	497	TTGACGAATTTGGTGAGCAAAATTAGTCATTTGGTTCAAAACTACAAATAATCAAAAGCT	556
OY	587	ctcttaataaggaacaagctgcacaacttaat---ttcttaaaacaacttggct	643
Db	557	TAGGACTTTAGAGAGCAAACTCAAAAATATGCTGTGACCTTAAAGCTGGCGTGGTT	616
OY	644	tggaataactactgatttctacatgaagcattctgcagcttcttgagcgagataaa	703
Db	617	TAGATGTTATCTCAGGGCTATTATCGGGCGCAACAGCTGCACCTTGACTTGACATATAAA	676
OY	704	atgcatcgcattgycaaaaaagctgcgcgcaggttttgaattaaagcaatcaattatgta	763
Db	677	ATGCTTCAACAGCTAAAAAAGGTGGGTGGGTTTGAATTTGGCAAAACAGTTGTTGTA	736
OY	764	atgtacaacaagaacttctctcaatglttttagcacacagctgtcgtcgtgtctataca	823
Db	737	ATATTACCAAGCGCTTCTTCTTACATTTTATGACCCAAAGCTTTCACAGAGTTATCTT	796
OY	824	ctaattgtgcgttgcgtcttaacttaactcaatgatactgtcttgcaattagctcttgg	883
Db	797	CACGTGGCGCTGTGGCTGCTTATATTTGCTTACTGTTTCTCTTCGANTATGCCATTAG	856
OY	884	catttaegaatgacagataaataccaatcagtcatactcctctgatagttgcgaaac	943
Db	857	CATTTCGGCGTATTTCGGCAATAATTAAATCATGCAAAAAGTTAAGAGTTATGCGCAAC	916
OY	944	aattcgcgaaaacttgcctatgatatgggatcattatctgctgcgaatacaacgctggtg	1003
Db	917	GCTTTAAAAAATTAGCGTATAGCGTAGAGGATAATTTATACAAATAATACGCGGGACAG	976
OY	1004	gtactatctgaagcttcaataacataatagtagagcattagtcagttctctgcttgg	1063
Db	977	GGACTATTGTATGCAATGCGTTACTGCATTTAATACGCATATGGCCGCTATGTGCTGGTG	1036
OY	1064	tttcgcgtctgcctgttagagatcgtcgttctgtgcgcagatctcacattagttgcaggt	1123
Db	1037	TGCTGCTGCTGGAGCGCGCGTGGTATTGCTTCAACCACTTCCTATTATAGATCTGSGA	1096
OY	1124	ttacagatgtatcctctgtaatttagaagcgtctaaacaggcaatglttgaagtgtg	1183
Db	1097	TTACCGGTAAATTTCTACAGATTCCTGCATATTCTTAACCAACCATGTGTGGACGCTTG	1156
OY	1184	ctaacgcttcaacagyltaaaattttagagtggggaaagaacaaatgycgttcagaactct	1243
Db	1157	CAAAATAAATTCATACAAAAATGTGAAATGGAAAAAATATATACGCTAAGAACTACT	1216
OY	1244	tgtgtaaaagcctatgattctcgttatgcgtcttactatagcttaactaaatttgtt	1303
Db	1217	TTTGAATATGGTTTACGATGCCCGCTTATCTTGCCGAATTTACAGATATATATGAATTTCTAC	1276
OY	1304	ctgaagctaaataaagatltggaagcgtgaacggttatttgcacatccacaacaacgltgg	1363
Db	1277	TGAACCTTAAACAAAGATTTACAGCGAGAAAGTGTCATGCTATTACTCAGACGAAATGG	1336
OY	1364	ataataatatgtgtgagtttagcaggtataccaatltggtgtgaacgcatlaagacggaa	1423
Db	1337	ATAACCAACATTTGGTATTAGCTGTGATTTATAGCGCTTTAGGTAAAAAGCTCTTACTGCTA	1366
OY	1424	aagctttagcagaagcttcttgaaatgtaggaagaagaatltgaagctgtgtccaatatact	1483
Db	1397	AAGCTTATGTGGATGCTTTGAAGAAAGGCAACACACTTATAACCCATATAATTTAGTACACT	1456
OY	1484	tggaatgctaaacatggtatcatatagacatltgaatctcaaatltggaataaagacgcaagct	1543

Db	1457	TGGATTTCGGCAAAACGGTATTATGTAGTGTGAGTAATTCGGGTTAAACCGAAACCTCAGCATTA	1516
Qy	1544	tgcatcttaacttgcgctcttgtaacaagcaggaactgaaatcaacgttgaacttaactg	1603
Db	1517	TCTTTTGAAGAACGCCATTATTGACGCCGGGGAACAGACATCTGTAAACGGCTACAAACAG	1576
Qy	1604	gtaaatactcttataltaataagttaaataatcgcagctgtaaaaaaactgcgaagttaacg	1663
Db	1577	GTAATATGAAATATATTTATACCAAGCTCAATATTAAACCGTGTAGATAGCTGAAAAATTACAG	1636
Qy	1664	atgcgaagcgtaagttcttaaatagaattctcttaagaagttaactcaagctgttagccgaagaag	1723
Db	1637	ATGGTGACGACAAAGTCTACCTTTGATTTAACTAACAGTTGTTTCACGGTATGTGATTTGAAT	1696
Qy	1724	aagcgacagacgcagatctgctctcaactagtaaatgcaaaa-----g	1762
Db	1697	TAGACAAATCTGTGGAATATGTAACTAAACCAAGAAACAAAAATTTTGCCAAACTTGGTG	1756
Qy	1763	ctgcgaatgacagatalcttctgtgtgcaagyltaaaatgaaatltgaatgtgtgcgaatgagac	1822
Db	1757	AAGGTGATGACAAACATTTTGTGTGGTCTCGTACACAGCAAAATGTATGGCGGTAAAGGTT	1816
Qy	1823	acgaatcgtgtctctctatgttaaagccggaagatttgcgtaattcttcytlagatgtgaaga	1882
Db	1817	ACGACCGAGTTCACATATAG--CCGTGGAAACATAGGTGCTTTAACTATGTGACAAACA	1873
Qy	1883	gtgcacaagaagcagcagatltatagaatcaactgcgtaagcttgcctgaagtgtatctaac	1942
Db	1874	AAGAACACCGAGACAGGTAGTTTACCGTTAAATCGTTTGCTGACAAACCGGTAAAGCATAC	1933
Qy	1943	atgaagctgtgtgaagcgtcaagaagaccaaagctgtgttaaaactgtaactaactccagatc	2002
Db	1934	ACGAATGTGACTTCAAACCCATACCGCATTAGTGTGGCACAACCGTGAAGAAAAATAGAAATATC	1993
Qy	2003	gtgattatgaatlaaagaaagtctgtgtatgttaccagtctaacgataattgaaataag	2062
Db	1994	GTCATAGCATATACACGACCCATG--CCGGTTATTATACCAAAATATACCTTTGAAGAGTG	2050
Qy	2063	tgaagaagatattgttctcaatlaatgaatgatactcaaaagcttcaatcaactgaagca	2122
Db	2051	TTGGAAGAAATTTTCGGTACATACATTAACGATATCTTTTAAAGGTAGTAAGTTCAATGATG	2110
Qy	2123	tattccataatgtgtgaaggtgtatgttaactgcagatgtgtgtgcgtgcgagacgcgctgtg	2182
Db	2111	CCTTTAACGGTGTGATGTGTGCATATATTGACGGGTAAACGAGGCATGACCGCTTAT	2170
Qy	2183	ttgtgtgttaagaagcagacgactctctgcgaatgaaagcgatattactctcgatgagc	2242
Db	2171	TTGGTGGTAAAGGCATGATTTCTTCGATGGTGGGAAATGGTCATATATTTATTCGATGGCG	2230
Qy	2243	gtctcgtgtgaatgattgataaaatgtgtgtgtgcgtgtaagtgtctatattcttgcgaaag	2302
Db	2231	GTAAGGCAACACCTATTACACGGGTGGCAAGGGGATGATATTTTCGTTACCCCTTAAG	2290
Qy	2303	gtgatgtgaatgatacttctgtacagatgtgcagcggcgcaatgataatgaactgtgcagatg	2362
Db	2291	GGGATGTGAATGATTTATTATTCGATTCGACAGGCAATGATTAATTTATCATCTCTGTGAT	2350
Qy	2363	caaatatattcgtatattatgtattgaaagcgtlaccaaagaggtattatgaattaaacgaatg	2422
Db	2351	CGAATCTTAAAGATTTAATCATTTTGAAAAAGTTAAACA--TAACTTGTGCATCACAGAAATA	2407
Qy	2423	atcatctcgtgtgtatttaacataccaagaatgtgtacataacatacaatttaacaaa-----	2477
Db	2408	GCAAAAAAGAGAAAGTGCACATTTCAAACCTGGTTCCGAGAGCGTGAATTTTTCCTTAAAGAG	2467
Qy	2478	---ttatcaagaagtataaacaagatacaaaatgtgaacaaactaaattgtgtlaaagaatgta	2533
Db	2468	TGGCTAATTTATTAACCACTAAAGATGGAAGAAATGGAAGAAATCATCGTCAAAATGGCG	2527
Qy	2534	gtatatacactccgatcaaatgtgataaaattt 2567	

Db	1277	TGAACCTTAACCAAGACTTTCACGGCAGCAACGTCGTCTACCTTTACTCAGACGCAATGGC	1336
OY	1364	ataataatcttggtgagctagcagcatttaccaaatctgggtgaacgcaltgaagcggaa	1423
Db	1337	ATAACAACATTTGGATTTAGCTGTGATTAGCGCGTTAGGTGAAMAAAGTCCTTAOTGSTA	1396
OY	1424	aagctctgcagatgctctttggaagaatggcagaagaagtgtgaagctggtccaaataactc	1483
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OY	1484	tggatgcataaacctgcatcatagacatcagtaattcgaatcgaatcggaaaaaacgcgaagct	1543
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OY	1544	tgcattcgaactcgcctcttgtaacagcagagactgaatcagctgtaacgtttaactaag	1603
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OY	1604	gtaaatcctcttataataaagaatctaataatcggacgcgtgtaaaaaactggcgaagtacag	1663
Db	1577	GTAATTATGATATTAATTAACCAACACTCAATATTAAACCGTGTAGATAGCTGGAAATTACAG	1636
OY	1664	atggagagcgctagttctcgaatctagatcttcctcgaagttatagcggtgtagccgaagacg	1723
Db	1637	ATGGTGACAGAACTTCACTCCTTTGATTTAACTAACGCTGTTCAGCGTATTTGGTATTGAAT	1696
OY	1724	aagcagacagacgagatcgtcctaactagtaaatgcaaa-----g	1762
Db	1697	TAGACATAGCTCGGAAATGTAACCTAATAAACCAAGAAACAAATAATTATGCCAAACTTGGTG	1766
OY	1763	ctggcaatgcagatctcttggtgcaaggtaaatgaaatgaaatctgactgtgtagatgagc	1822
Db	1757	AAGTGATGATCAACAGCTTTGTTGGTTCGTGACACGCGAAATTTGATGGCGGTGAAGCTT	1816
OY	1823	acgactgctctctataagtaaaagcggggagatctgtgtaatactactgtagatgtgaacg	1882
Db	1817	ACGACCCAGTTCACTATAAG---CCGTGGAAACATATGTCCTTTAACTATGATGACAAACA	1873
OY	1883	gtgcaacagaagcagcgagctatacagatcgaatcgtgaagtctgcaggtgatactaac	1942
Db	1874	AAGAGACCGACAGAGTAGTATTACCGTGAATTCGTTTCGTAAACACCGGTAAAGACATAC	1933
OY	1943	atgaagcttgtaagcgtctcaagaaacaaaggltggtaaacgtatctgaactatccagatc	2002
Db	1934	ACGAAGTGACTTCACACCATACCGCATTTAGTGGGCAACCGTAGAAGAAAATAGATATATC	1993
OY	2003	gtgaattctgaatgaagaagaagttgggtatggtatcatagctctacgcgaataattgaatcag	2062
Db	1994	GTCATACCAATTAACCAACACACATG---CCGGTTATTATACCAAAACATACCTTGAAGCTG	2050
OY	2063	tagaagaagaatctggtctcgaatttaagaatgtaagatcgaaggtcctaattcaaacgcga	2122
Db	2051	TTTGAGCAATTAATCGGTACTCATCATTAACGATATCTTTTAAAGTATGTAAGTTCAATGTAG	2110
OY	2123	tattccatagtggtgaaggtgatacttaactcgaatggtgtgtgtgtgtaacgcgcgtgt	2182
Db	2111	CCTTTAACGGGTGGATGGTGTGATACATATTAAGTATTAAGCGTAACGCGCAATAGACCGCTTAT	2170
OY	2183	ctgggtgtaaggaacacgaatcgaactctctggagatgaagaatgaacgaatgaatcctgaatgcg	2242
Db	2171	TTGGTGATTAAGGCGATGATATCTCGATGGTGGAATGCGATGATTTTATCGATGCGCG	2230
OY	2243	gtctcgtgtagtgaatgaatgaatggtgggtgcgtgtaatagtctatatactcttcggaag	2302
Db	2231	GTAANAGCAACGACTTATTAACAGGGTGGCAAGGGCGCATATATTTTCCTTACACCGTAAAG	2290
OY	2303	gtgaatgtaatgaactcttgtaacgtgagcagcggcgaatataataatgaatcttgacagctg	2362
Db	2291	GGCATGGTAATGATATTAATTACGGATTTTCGAGCGCAATATTAATTAATCAATTCCTGTGATT	2350
OY	2363	caaatatactgatatataatgaatgaaactgaacaaagggtatctatagttlaaacgaatg	2422

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Db 2351 CGAAGCTTAAAGATTTAACATTTGTAAGAAAAGTTAAACA---TAAATCTTGCATCGACGAATA 24
Oy 2423 atcaltcaggtagatataacataccagaatggtacatacaataaatttacaacaa-----247
Db 2408 GCAAAAAAGAGAAAAGTACACCTTCATAAACCTGTTCCGAGAGGCGTGAATTTTGCTTAAGAAAG 246
Oy 2478 -----ttatcaagaagtataaacaagatcataaatttgagcaactaatigtgtaagaatggtga 253
Db 2468 TGCCTAATTATTAAGCAGCTTAAGACTAGAAAATCGAAGAAATCATCGTCAAAATATGCGC 252
Oy 2534 gttatactccgatcaataatgataaaattt 2567
Db 2528 AGCGATCACCTCAAGCAAGCAAGTGTATGATCTTAT 2561

RESULT 10
US-08-535-837-1
; Sequence 1, Application US/08535837
; Patent No. 5985289
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: HARLAND, RICHARD J.
; TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PRO
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBERTA L. ROBINS
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,837
; FILING DATE: 27-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0026.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2794 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2778
; US-08-535-837-1

Query Match 29.3%; Score 814.4; DB 2; Length 2794;
Best Local Similarity 60.2%; Pred. No. 2.9e-177;
Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps

Oy 53 caaagctcgtgaattaaaaatcttacttggctatcccaagaat-----tatgacgcgc 106
Db 29 CAAAACATGGGGCAAAAAAAATATTCCTGTATATTTCCCAAAATATACCAATATGATATCTG 88
Oy 107 aaaaagtgtagaacttaatgaattttaaagctgctgtagaattagatgattgcgcgt 166
Db 89 AACCAAGGTAATGATTTCAGGATTTAGTCAAAAGCGCCGAAGAGTTGGGATTGAGAGTAC 148

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OY	167	tagaagaagcctaaatcaacacgaaacgcgaataaatcgtgtgacacgtaatacagtc	226
Db	149	AAAGAGAGAGAACCAATTAATATTGGCAACGCTCAACACCAAGTTTAGCGATTCAAACG	208
OY	227	ttcctctccacaacaacatcgtgatgtcattcttcgcacaacaatttgaanaagttctac	286
Db	209	CTATTGGCTTAACCTGAGCCGTGGCATTTGTGTATCCGGCTCCCAAAATTGATTAATTGGTAC	268
OY	287	aaaaacattccacaataagtttagccaaagggttagacagtgtagaanaattgatcgta	346
Db	269	AGAAA-----ACTAAAGCAGCGCCAGCATTTAGTGTTGTCTGCCGAAGCATTTGTACAA	319
OY	347	aattagtgtaagcaagtaatgatatatacaaatgaactccttlttttggcacctcatag	406
Db	320	ATGCAAAATTAAGCCAAAACGTAATTAATTCGGCATTCACATCTAATTTTAGCGCATCAATTTGG	379
OY	407	cgggtatagaacttgattcttctaataaaaaggatgctgacactgtagtcttggtcta	466
Db	380	CTGCAATGGATTATAGATGAGGCGCTTACAGAA---TACACGACACCAACATCTCTTGCTA	436
OY	467	aagctatattgacttgatthaatacgaataatttgtaactctatcctaagtaactcaacga	526
Db	437	AAGCTGCGTTGAGACTACAAATTTCAATTAATGAAATATTGCTAATTCAGTAATAAACAC	496
OY	527	ttgaagaacttctctcagctgtagcaagtttagtctctactatcgaagctaaagct	586
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OY	587	tctctaataatagaanaaagttgcaaaccttaaat---ttcttaaacaaatccttggt	643
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OY	644	tggaataatactagtggtttgcatacgaagatctctgcaggtctttagcggataaaa	703
Db	617	TAGATGTTATCTCAGGSCATTAATCGCGGCAACAGCTGCATCTTACTTCAGATATAAA	676
OY	704	atgcatacgcgcgcaaaaagatgtgcgcaggttttgaatlaagcaatcaagttatgta	763
Db	677	ATGCTTCAACAGCTAAAAAAGTGGGGTGTGTAATTTGCCAAACCAACAGTTGTGGTA	736
OY	764	atgtaacaaagcaattctctcatatggttttagacaacggtgtcgtcgtcatcaa	823
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Db	797	CAACGGGCGCTGGCTGCTTAATGCTTCACTGTTCTCTCGATTAAGCCATTAAG	856
OY	884	cattatagaatgcagcagataaatcaatcaatgcataatgcctgcataagtttgcacaac	943
Db	857	CATTTTGCGCGATTTGCCGATTAATTAATCATGCCAAAAAGTTTAACAGATTATGCCGAC	916
OY	944	aattccgaaaatttgctatgtagtggagatcattatattgctcctaataatacagtggtg	1003
Db	917	GCTTTAAAAAATTAAGCTATAGCGGAGATTAATTAATTAACAAATATACGGGGGAACAG	976
OY	1004	gtactatagaagcttcatcttaacataattagtaacgcataagtgtaagttctctgctgtg	1063
Db	977	GGACATTAATGAGCATTCGGTTACTGCAATTAATTAATTCGCCATTTGGCCGCTATTTGCTG	1036
OY	1064	ttccgcgtcgtcgttagagatcgtcgtgtgtgtagcagatgtgcactatagttcaggtg	1123
Db	1037	TGTCTGCTCGTGCAGCGCGCTCGGTTAATGCTTACACCGATTCCTTTATTAATCTGSGA	1096
OY	1124	ttacaggaattgactctcgggaatttttagaagcgtctcaaacagcgaatgtttgaagtgct	1183
Db	1097	TTACCGGCTGTAATTTCTACGATTTCTGCAAATATTCTAAACACCAATATGTTTGACACGCTG	1156
OY	1184	ctaacccgtttacaagtaaaaattttagagtgagtggaagcaaatgvcgctgacgaactt	1243
Db	1157	CAATAAATAATCATTAACAAAATTGTAGATGGGAAAAAAATATATACGCTGAAGAACTACT	1216
OY	1244	ttgataaagcgtatagcttcgttatgctgtcgtctatttagcttaacttaaatatttgtt	1303

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Db	1277	TGACCTTAACAACAAGAGTTATACACGACGAGAACGHTCATCGCTATTACTACAGACGAATGGG	1336
Qy	1364	ataataatttgtagttagcaggtattaccaaatitgggtgaacgcgttaagacggaa	1423
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Qy	1424	aagcttctgcaagatgcttttgaagaatggaaagaagttgaagctgtgttccaatltactt	1483
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Qy	1484	tggatgtctaaacatggtatcatagatagatagtttaattccaatttggaaaaaacgcgaacgt	1543
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Qy	1544	tgcatttcaacttgccttgttataacagcaggaacttgaatcacgtgaacglttactaatg	1603
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Qy	1604	gttaatactcttataatgaatgaatgaatgtggaagctgttaaaaaacgcggaaattacag	1663
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Qy	1664	atggaagagcttagttcttaaatatgatttcttccaagttaattcaagcgtttagcggagaaag	1723
Db	1637	ATGTTGCGACGAACTGTACTCTTTGATTTAACTAAGCTTGTTCAGCGTATTGTGTAATGAT	1696
Qy	1724	aagcagacagagatgtgtctataatgttaatgcaaaa-----g	1782
Db	1697	TAGCAATGCTGGAATGTACTTAATTAACCAAGAAACAAATAATATTGCCAACTTGCTG	1756
Qy	1763	ctggcaatgacagatatcttgggttggccaaggttaaaatgtatattgattgtagagatgac	1822
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Qy	1833	acgaatcgttcttcatagtaagaacggaggaatttggtaataattactttagatgtgtgca	1882
Db	1817	ACGACCGAGTTCACTATAG---CCGGGAACATGATGCTCTTAACTATTGATGACACCA	1873
Qy	1883	gtgcaacagaagcagcagcattatacagttatccgttaatccgtatcgtccgaggtgatatcc	1942
Db	1874	AAGAGACCGACAGCATGATTATACCGTAAATCGTTTCTGTAAACACCGTTAAACGACATAC	1933
Qy	1943	atgaagtgttgaagcgtfccaagaacccaaggttgaagaatgaatgaacttccaatccagttc	2002
Db	1934	ACGAAGTCACTTCAACCCATTAACGCGCATTAATGGGCAACCGTAAAGAAATAATGATAATTC	1993
Qy	2003	gtgattatgaaatlaagaanaagcttgggtatgttattatcaagcttaccgataatttgaatatag	2062
Db	1994	GTCATAGCAATTAACACACACCATG---CCGGTATTACACCAAAAGTATCCTTGAAGAGTG	2050
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Db	2051	TTGAAGAATATTATCGTACATCATTAACCATATCTTTTAAAGTATGAATGTCATGTATG	2110
Qy	2123	tattccatagtggtgaaggtgatatgtattactcgatgtgtgtgtcgttgaagcagcgctgt	2182
Db	2111	CCATTAAACGGTGGATGGGTGCGATATTAATACCGGTAAACAGCGCAATGACCGCTTAT	2170
Qy	2183	tttgtgtgaagaagcaacgtacgacttcttgagatgaagaagcatgatttaacgtatggc	2242
Db	2171	TTTGGTGTAAAGGCGGATATTTCTGATGTGTGGAATGTGATGATTTTATCGATGAGCG	2230
Qy	2243	gtctcgtgtaatgtaataatggtgtgtcgttgaatagtatctatacttctggaaag	2302
Db	2231	GTAAGGCAACGACCTATTATACAGGTGGCAAGGCGCATGATATTTCGTTCACCGTAAG	2280
Qy	2303	gtgagtgaatgatacttgtacgatgtgcaagggcaatgaataatgaatcatttgcagta	2362

Db	2291	GGCATGTGTAATGATATTATTACCGATTCTGAGCGCATGATAAATTATTCATTCTCTGATT	2350
Qy	2363	caatatatctgatatatbataatgtgaacgacccaagaaggatcttatagttaaacaagaa	2422
Db	2351	CGAAGCTTAAAGATTTTAAACATTTTGAAAAAGTTTAAACA--TATCTTGTGCATCAGATA	2407
Qy	2423	atcatcaggtagatataacataccaagaatgtgtacatacatcaattcaaaaa----	2477
Db	2408	GCAAAAAAGGAAAGTGACCATTCATAACTGGTTCGAGAGGCTGATTTTGCTAAAGAG	2467
Qy	2478	----ttatcaagtaataaacaagatcatataaattgagcaactaaattgtaagaatgtta	2533
Db	2468	TGCCTAATTATTAAAGCAACATTAAGATGAGAAATGCAAAATTCATCGTCAAAATGCG	2527
Qy	2534	gttatatacacttccgatccaattatgataaaatttt	2567
Db	2528	AGCGGATCACTTCAAAAGCAGAATGGATGATCTTAT	2561

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RESULT 11
US-09-124-491-5
Sequence 5, Application US/09124491
Patent No. 6022960
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANN, JOHN G.
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,491
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2794 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2778
US-09-124-491-5

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Query Match	29.3%;	Score 814.4;	DB 3;	length 2794;
Best Local Similarity	60.2%;	Pred. No. 2.9e-177;		
Matches 1538;	Conservative	0;	Mismatches 956;	Indels 60; Gaps 9;

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OY	107	aaaaagctggaacttaaatgatttataaagctgcatgaatagatgatctgcgt	166
Db	89	AACAAGTAATGCTTTACAGACTTTAGTCAACGGGCCAGACAGTTGGGATTTAGAGTAC	148
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OY	227	ttctctctccacaacaacagtgatgtgctatcttcgcacaanaattagaagaagctctac	286
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OY	287	aaaaacatctcaccaataagcttagccaagaagcttagacagagctagaaaaatctga	346
Db	269	AGAAA-----ACATAAGCAGGGCCAGACATTAGCTTCTGCCAAAGCATTGTACAA	319
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OY	407	cgggtatagaacttgatctcttaatacaaaaagtgatgctgacagtaagcttgctgta	466
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OY	467	aagctagatattgacttgatttaataagagataaattgtaatactatactcaagatctaacaaga	526
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OY	527	ttgaagcatttctctccagcttagcaaaagttaggttctactatactgcagagctaaagct	586
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OY	587	tctctaataaggaacaagctgcaaacacttaaat---cttcttaaaacaactcttggt	643
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OY	644	tggaataatactagtggttctgatacagcgcaattctgcaagctctgcttagcgaataaa	703
Db	617	TAGATGTTATCTCAGGGCTATATATCGGGGCCAACACCTGCACCTTGACTTGACATATAA	676
OY	704	atgcaactgcactgcaaaaaaagtctgcgcagagctttagaattgaagcaatacaagtattgta	763
Db	677	ATGCTTCAACAGCTTAATAAAAAAGTGGGGTGGGCTTTGCAATTTGGCAAAACAAGTTGTTGTA	736
OY	764	atgcaacaagaagaactcttctcaatgatttagacaacaagctgtgctgctgctcatcaa	823
Db	737	ATATTACCAAAAGCGCTTCTTCTTACATTTTAAACCCCAACAGTGTGCAGCAGGTTATCTT	796
OY	824	ctactggtgcgtgtgctgcttaatactactcatcgatattgttggcaattagtccttgg	883
Db	797	CAACTGGCGCTGGCGCTGCTTAATTTAGCTTCTACTGTTTCTCTTCGATTAATACCCATTAG	856
OY	884	catltagaatgcaagagataaatacaatcatgactgaatgctcttgatgatgttgaanaac	943
Db	857	CATTTCGCCGATTTGGCCGATTAATTTAATCATGCAAAAAAGTTTAAAGAGTTATGCCGCAC	916
OY	944	aattccgaaaaattgctgatagaaatgggaagcaattatctgctgaatacaacgctgtgtg	1003
Db	917	GCTTTAAAAAATTAGCCTATAGCAGCGAGTAATTTAATNACAAATATCAACGGGGCAACAG	976
OY	1004	gtactatctgaagctcaataactacaattagtaaggcaattagtgagctttctgctgtg	1063
Db	977	GGACTATGTAATGATCGGTTACTGCAATTAATNACCCATGAGCCCTTATTCGTGTGTGTG	1036

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QY	1124	tttaagaattgtaactctgcgaatttcttgaagcgtctcaacagcaatgctttgaagttgtg	1183
Db	1097	TTACCGGTGTAATTTCTACGATTCTGCATATTCTTAACACAGATGTTTAGACAGCTTG	1156
QY	1184	ctaacgcttccaaaggtlaaaatttllagagttgggnaaagcaaaatltgcygltgaagacatt	1243
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Db	1217	TTGAAATGGTTTCAGATGCCCCGTTATCTTGCCAAATTTACAAATATATATGAAATTTCTAC	1276
QY	1304	ctgagctcaaaataaagagtttgaagctgcgaacgcygtatttgcgaatccacccacaagaactgg	1363
Db	1277	TGAACCTTAAACAAGAGGTTACAGGACGAAACGHTCAATGCTATTACTAGCAGCAATGGG	1336
QY	1364	ataataatcttgtagttagtgcagcgattaccacaatltgggttgaacgcattagaacggaa	1423
Db	1337	ATACAACAATTGGATGATTAGTCGTGATTAAGCGCGTTTGAAGTGAANAATCCTTAGTGTTGA	1396
QY	1424	aagctatgcagatgcttcttgaagaatgcgaagaagaattggaagctggttccaaattactt	1483
Db	1397	AAGCCTTATGCGATGCGTTTGAAGAGGCAACACATTAAACCCGATTAATTAATACAGT	1456
QY	1484	tggatgtctaaactggtatcatatagaacattagtaatttcaaattgggnaaaaaacgcaagcgt	1543
Db	1457	TGGATTTGGCAAAACGGTATTATGATGTAAGTAATTCGGGTAAACGGAACCACTACAGATA	1516
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Db	1517	TCTATTTCAGAACCCCTTATTTCACCCCGGGACAGACAGATCGTAAACCGCTACAAACAG	1576
QY	1604	gtaaatactcttatbathaagaattaaatltcgcagcgtgtlaaaaaactgcgaagttacag	1663
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QY	1664	atggaagagcgtagtttctaattcgaattcctctcaagttatcagcgtgttagccgaagacag	1723
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Db	1697	TAGACATGCTGGAAATGTACTAAACCAAGAAAGAAACAAATAATTTCGCCAACTTGCTG	1756
QY	1763	ctggcaatgcagataltccttgtgtgtcgaaggtaaatgtaatatttgaatgtgtgagatgac	1822
Db	1757	AAGTGTGATGCAACAGTATTTGTTGTTCTGTGTAACGACGGAATTTGATGGCGGTCAAGGTT	1816
QY	1823	acgatgtgtcctctatagtaaagaecggagagatttggtaataatactctgttagatgtgta	1882
Db	1817	ACGACCCAGTTCACCTATAG---CCGTGGAACACTATGTCCTTTAATCTTTATGATCAACCA	1873
QY	1883	gtgcacaagaagcagcgagatataagaattcaactcgttaaggtgtcaggtgatatactaac	1942
Db	1874	AAGAGACCGACAGAGGATTTATACGGTAAATCGTTTCTGTAAACACCGGTAAAGCACTAC	1933
QY	1943	atgaagttgtgaagcgttcaagaacaagaattgtgttaaagcttcaacttcaagatctc	2002
Db	1934	ACGAAGTGACTTCACACCCATACCGCATTTAGTGGGCAACCGTGAANAATAAATAATAGATATTC	1993
QY	2003	gtgatattgaattaaagaagaattgggtatggtatcagtciaacgcgaatttgaattcag	2062
Db	1994	GTCATATCAATAAACACACACCATG---CCGGTATTATACACCAAGATATCTTGAAGGCTG	2050
QY	2063	tagaagaagaattgtgttctcctaatttaaigtatattcaagaagttctaaattcaacagaca	2122
Db	2051	TTGAAGAATAATTATCGTACTTCACATTAAGCATATCTTTAAAGTATAGTATGATCATGTGT	2110

Oy	2123	taltccatagtggtgaagagtgatgatttaactcgtatggtgtgtgtgtgtgaacacgctgtt	2182
Db	2111	CGTTTAACGGTGGGATGGGTGCGATATCTATTTGACGATACAGCGCAATATACGCTTAT	2170
Oy	2183	ttggctggaaggaacagatcagactcttcgtgagatbaagcgatataactcogatgcg	2242
Db	2171	TTGGTGGTAAAGGCGATGATATCTTCGATGATGGAAATGCTGATGATTTTATTCGATGGCG	2230
Oy	2243	gtctctgtagtatgatatataatggtgtgtgtgtgtgaatgattctatattccttggaaag	2302
Db	2231	GTAAGGCAACGACCTATTTACAGGGTGGCAAGGCGCATATATTTTCGTACCGCTAAG	2290
Oy	2303	gtgattgtaattgactcttgcactgtgcagcgcaatgatatattgacatttgagatg	2362
Db	2291	GGCATGTGATGATATATTATTCGAGATTCTGACGGCATATATAATTATTCATTCTCTGATT	2350
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RESULT 12
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; Patent No. 5476657
; APPLICANT: POTTER, ANDREW A.
; TITLE OF INVENTION: PASTEDURELLA HAEMOLYTICA LEUKOTOXIN
; COMPOSITIONS AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/15,537
; FILING DATE: 09-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 504,850
; FILING DATE: 05-APR-1990
; APPLICATION NUMBER: 335,018
; FILING DATE: 07-APR-1989
; SEQ ID NO: 2:
; LENGTH: 2794
5476657-2

Query Match	29.3%	Score 814.4	DB 6	Length 2794
Best Local Similarity	60.2%	Pred. No. 2.9e-177		
Matches 1538	Conservative	0	Mismatches 956	Indels 60
			Gaps	9
QY	53 caaagctcgtgataataaaatcttaacttacttcgtgcatccccaagt-----tatgatacgcg	106		
Db	29 caaaactcgtgggcacaaaaaattatccctcatctattatccccaattacacatatgtatcgc	88		
QY	107 aaaaagctggagcaatttaatttataaagctgctgataatgattgtatgtctgatt	166		
Db	89 aacacaggtatcgtttacacggaatttagtcaaaagcggccgaagagcttggatattgagttac	148		
QY	167 tagcgaagaagcgtatcacactgacgaacgcgaacaaaatctgtacacagtaaatcagt	226		
Db	149 aaagagaagaagcgcataatatctgacacagcccaaccagtttagcagatccaacgcg	208		
QY	227 ttctctctctcacacaaactggtattgtctatttctgacacaaattagaaaaagtctctac	286		
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OY	287	aaaaacattctaccaataaagtgtgccaagaaggttgagacggtgtlagaataatctgtcgt	346
Db	269	agaaa-----actaaagcagcgccaaacatctatggcttcgcgaagcattgtcaaa	319
OY	347	aattaggctaaagcagaataagtctatccaacattaaagcctcttttggccactgattag	406
Db	320	atgcataataaagccaaaacgttatattctgycatctcaatctattttagctccagattgg	379
OY	407	cgggctatagaactctgattctcttaactcaaaaagtgatctgacactggtctctgtgcta	466
Db	380	ctggaaatgagatttgatgagcgcttacaaga---taacagcaaccaactgctcttgcta	436
OY	467	aagctagtatctgactctgattaatgagataatggttaactctatctcagagtactacaaga	526
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OY	527	ttgagagactttcttcacagtttagcgaagtttaggtttctctatctatocgagctaaagct	586
Db	497	ttgcgcaatttgtgtgagcaaatctagccaatttggttgcctcaaacacataccaagctc	556
OY	587	tcctaaatagagaaacaagttgcaaaacttaaat---cttctcaaaaacaactgttgt	643
Db	557	taggagactttagagagacaacatccaaaaatactggtgactctgtataaagcttgcttgct	616
OY	644	tggaaataactactgctgttctcatcagcattctcgcagcgtcttgcttttagcgsataaa	703
Db	617	tagatgttatctccaggcctctatctcggcgcaacagctgactcttgacttgcagataaa	676
OY	704	atgcatacgcgsgaaaaaagctgtgcgcaggtttgaattaaagcaatcgaatttgtta	763
Db	677	atgcctcaacgcctcaaaaaggtgggtggtgttgaatttgcaaaccaagtttgttgta	736
OY	764	atgtaacaaaagcaactctctctcaatgtttaaacaacaagttctgctgtgtccataa	823
Db	737	atataccaaaagccggttctctcttacaattttagcccaagctgttgcaagagttatctt	796
OY	824	ctactggtgctgtgtcgtcttaactatctcatcgtataatgtttggaattagtccttgg	883
Db	797	caactggtgcctgtgcgtcttattgtctctactgttctctcttggaattagccattag	856
OY	884	cattatagaatgacgcagcataaattccaatcatgctaatgtctcttgatgagtttgcaaac	943
Db	857	catttgcggtatgctcgcaataaattcaatcatgcaaaaagtttagagaatttagccgcac	916
OY	944	aattccgaaaattgttgatgacgtggagatcatttatgttgcaatatacgcgtgtgtg	1003
Db	917	gctttaaataaatttagcgctatgacgcggagataatttatattagcagaataatccagcgggaaca	976
OY	1004	gtactattgaagcttcaattactacaattagtagtcggcatttagtgcagtttctgtgtg	1063
Db	977	gactatttgatgcatcgtgttactgcgaattataacgcgatttgcgctattgtgtgtg	1036
OY	1064	tttcgcgtcgtcgtctgtaagatcgtcgtgtgtggcgcagcttgcaattatagttagcagtg	1123
Db	1037	tgctgtgctgcgtgcgcgcgtctggtatgtgtcttccacgcgattgccthatagtatctgga	1096
OY	1124	ttacagagattgactctcggaattcttgaagcgtctcaaacagcgaattgtttgaagtggt	1183
Db	1097	ttaccggtgtcaattctcagatctcgcgaattcttcaaacagcaatggtttgagcaagctg	1156
OY	1184	ctaacgcttacaagytlaaaatttttagagttgggnaaagcaaaatgctgcgcgaactt	1243
Db	1157	caaatataaattctaaacaacaattcttagaattgggaaaaaataatacagtgtaagactact	1216
OY	1244	ttgtataagctatgattctcgctttagtgcgtctattttagctataactaaatttttgt	1303
Db	1217	ttgtaaaatggtttagcagatgcgcgttactctgtgcgaatttcaagaatataatgaaattcttac	1276
OY	1304	ctgagctcaaaataaagagtgtgaaagcgtgaacggtgttttccaatcccaacaagtggtt	1363
Db	1277	tgaactcaaacagaaggtctacagcgccagacgctgcatcgtctattctcaagcgaatggg	1336
OY	1364	ataataatcttggtagtttagcaggtattaccaaatgttggtlaaogctlaagaacgga	1423

Db	1337	ataaacaactggtggaacttcagctgtgatacttgaccggtcttaagtggaanaagtccttaagtga	1366
QY	1424	aagctatgagagatgagcttttggaaagatgagcaagaagtctgaactgtgtccaatattactt	1483
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Db	1457	tgatttcggcaaacggtatattatgtatgtgtgaattcctggtaagggaaaactcgacata	1516
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Db	1517	tctatttcaagaacgcacattatlgacgcgggaaacaagacatcgttgaacgcgtatacaacag	1576
QY	1604	gtaataactcttatattaattaagaattaaatctggagcgttlaaaaaacttgcgaattacag	1665
Db	1577	gtaatatgataataatattaccagaagctcaatacttaacggttgaatatacgttggaaaattacag	1633
QY	1664	atggaagagcagcttctcaaatatgaattcttcttaagaattlaacagcgttgaacgcgaacag	1722
Db	1637	atgtgtgcagcaagttctactacttggatttaactaagctgtgtcagcgtatgttatgtat	1696
QY	1724	aaggcacagacgagattgtgtctataagtaaatgcaaa-----	1762
Db	1697	tagacaatgctggaatactgtaacttaaaaccaaagaacaaataattgcacaaactgtgt	1756
QY	1763	cttgcaatgagagatattcttgtgtgtgaagaagtataatgttaatttgggttggaagtgac	1822
Db	1757	aaggatgagaacaagaactctgtgtgtgtgtgatacgcgggaatatgtgtgcggtggaaggt	1816
QY	1823	acgatcgtctctctataagaagaacggaagatttggtaatactactgtatgatactgtgaag	1882
Db	1817	acgaacgagttccactatag---ccgttggaacatctgtgttctaactattgatacaca	1873
QY	1883	gtgcacaagaagcagcagctatatacagtttaactcgttaaggttgcctcgaagttgatatc	1942
Db	1874	aagagaccgagcaaggtagttataccgtataatcgtttcgtgaagaacggtlaaagacatac	1933
QY	1943	atggaagtgtgtaagcgttcaagaacccaaggttgggtlaaacgtactgaactatccgattc	2002
Db	1934	acgaagtgtacttcaaccataccgacatagtggtggcaacggtgaagaaaaaatagataatc	1993
QY	2003	gtgatattgaaatlaagaanaagtttgggtatgtgtatcaagctctcaagataatttgaatac	2062
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QY	2063	tagaagaagtaattgttcttccaatttaatgatactatccaagaagtttcaaatccaacga	2122
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QY	2123	tattccatagtggtggagaaggtgatacttactcgaatgtgtgtgtgtgtgcgcgcgctgt	2182
Db	2111	cccttaacggtgtgtgtaatgtgtgtcgtatctatltgaacgtlaacgaacgaacgttgccttat	2170
QY	2183	ttggtgtlaaaggtgaacagatcgaacttctcttgaaatgaagaacgatactgaatccgcgtg	2242
Db	2171	tttgtgttgaaggtgagatactctcgaatgtgtgtgaatgtgtgtatcttaacgtgtgcg	2233
QY	2243	gtctctgtgtaatgatacttaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2302
Db	2231	gtaaggaacacgacctatttacaacgtgtgcgaaggtgagatatttctgtccgcgtlaag	2299
QY	2303	gtgatgtgataatgaacttttgaatgtgtgcgcggtgcaatgataataattgacattgcagatg	2362
Db	2291	gcgagtgttaatgataatattacacgattctgtgcaggtcaatgtataataattatcttctgtat	2350
QY	2363	caatatatactgataattatgattgaacgtgaccaaagaaggttatatagttaaagcaaatg	2422
Db	2351	cgaacttaaaagatttaactttgaaaaagttaaaaa---taattctgtatcaacgata	2407
QY	2423	atcatcaggtatgatttaataatacaagaatgtgtataataacatcaaatcttaaaaa----	2477

OY	1304	ctgagcctaaataaagagtttggaagccggaacggtttatccaatctgggttaaacgcatlaagaagcgga	1423
OY	1277	TGAACCTTAAACAAGAGATTACAGGCGAAGAGGTCTCCCTATTTACTACAGCAGCAATGG	1336
OY	1364	ataataatctggtgagtttgcagcagatataccaacttgggttaaacgcatlaagaagcgga	1423
Db	1337	ATAACACAACTTGGGATTATAGCGGTATTAAGCGCTTACGTAAAAAGTCCCTACGTGTA	1396
OY	1424	aagctatgcagatgctcttgaagatgcaagaagaattgaagctggcttccaatattact	1483
Db	1397	AAGCCTATGTGGATGCGCTTTGAGAGAGCGCAACACTTTAAACCGCATTAATTAGTACGT	1456
OY	1484	tggatgtctaaaacctggtatcatatagatattgaatttccaatggtggaaaaaacgcgaagct	1543
Db	1457	TGGATTTGGCAACCGGTATTTAGTGAAGTGAATTCGGGTAAAGCGAACTCAGCAT	1516
OY	1544	tgcattccacttcgccttctttaaacgcggaagctaaatccaagttaaacgtttaaactaag	1603
Db	1517	TCTTATTACAGAACCCATTATTACGCCCGGGAACAGACATGCTGACGCCATCAACAG	1576
OY	1604	gtaaatacctctatbathtaagaatlaaaatcggagcgttlaaaaaactgcgaagttacag	1663
Db	1577	GTAATATATGATATATATATACCAACCTCAAAATTAACCGTATGATAGCTGAAATTAACG	1636
OY	1664	atggaagagcgtagtcttccaattgatattctctcaagttatccaagtttlaagcgttgcggaag	1723
Db	1637	ATGTGTGACGAGAAGTCTTCACTCTTGATTATTAACTAACCTGTTCAGCGTATTTGGTATTGAT	1696
OY	1724	aagccacagacgagatggtgtctaatagttaatgcaaaa-----g	1762
Db	1697	TAGACATATGCTGGAAATGTACTTAAACCAAGAAACAAAAATTTATGCCAAACTTGGTG	1756
OY	1763	ctggcaatgacgaatctcttctgtgtcacaagtgaaatgaaatlgatgtggtgaagcga	1822
Db	1757	AAGGTGATGACAAAGCTATTGTGTGGTTGCTGACGACGGAATTTGATGGCGGTGAAGCTT	1816
OY	1823	acgatcgtgtctctatagtaagaagcggaggaattggtataatctacctgtagatgtgaca	1882
Db	1817	ACGACCGAGTTCACTATAAG---CCGTGGAAACATATGTCCTTTAACTATGTATGACACCA	1873
OY	1883	gtgcaacagaagaagcgagatatacagtttaactcgttaagttgtctcgaagtgaatctacc	1942
Db	1874	AAGAGACCGACGAAGGTAGTTATACCGTAAATTCGTTCTACAAACCGGTAAAGCATAC	1933
OY	1943	atggaatcttgaagcgtgtcaagaaccaaaggttgggtlaaacgtatctgaactaccgaatc	2002
Db	1934	ACGAAGTGACTTCAACCCATACCGCATTTAGTGGCCACCGTAGAAGAAAATAGATATATC	1993
OY	2003	gtgattatgaaataagaagaagttgggtatggttatacagttctacgataatctgaatccag	2052
Db	1994	GTCATACCAATTAACACACACCATG---CCGCTTATATACCAAAATATCCTTTGAACCTG	2050
OY	2063	tagaagaagaatagtgtcttccaatttaagatgatatccaagaagttcttaattcaacgcga	2122
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OY	2123	tattccatagtggtgaagagtgatgatttaactcgaatgtgtgtgtggaacgcgcctgtt	2182
Db	2111	CCTTTAAACGGTGGATGAGTGTGCGATACATATTGACGGTAAACGCGCATAT	2170
OY	2183	ttggtgtgtaaaagcaacgatcgacttctcgtgagaagaagcgaatgaattactcgaatgcg	2242
Db	2171	TTGGTGTGTAAGGCGATGATATTCGTGAGTGTTGGAATGTGATATTTATTCGATGCGCG	2230
OY	2243	gtctctgtgtagatgattttaaagtggtgtgtgtgataatgtctatctcttcggaaag	2302
Db	2231	GTAAGGCAACGACCTTATTAACAGGTGGCAAGGGCGCATATATTTTCGTACCCGTAAAG	2290
OY	2303	gtgagttaatgcatcttctgacatgacgcggcgaatgataaatatgacttgcagatg	2362
Db	2291	GGCATGTGAATGATATTAATTACGAGATTTGACGGCAATATATAATTAATCATTTCTTGATT	2350
OY	2363	caaatatctgbatatlatgattgaacagtaaccaagaaggttatatagtttaacgaatg	2422

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Db	2408	GCAAAAAAGGAAAGTGACCATTCAAAACTGGTTCCGAGAGGCTATTTTGGCTAAAGAC	2467
Qy	2478	-----ttacaagtaataaacagatcatcaaaatgagcaactaa ttgtaaga ttgta	2533
Db	2468	TGCGTTATTTTTAAAGCACTAAAGATGAGAAAAATCGAAGAAATCATCGGTCAAAATGGCG	2527
Qy	2534	gtatacacttcgcgatccaattgataaaattt	2567
Db	2528	AGGGGATCACCTCAAAAGCAAGTTGATGATCTTAT	2561

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RESULT 14
US-08-455-970A-11
Sequence 11, Application US/08455970A
Patent No. 3708155
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P. A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
TITLE OF INVENTION: CHIMERAS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: REED & ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,970A
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2817 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2808
US-08-455-970A-11

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	Query Match	29.3%	Score 814.4	DB 1	Length 2817
	Best Local Similarity	60.2%	Pred. No. 2.9e+177		
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Qy	53 caaagctcgtgattaaataacttactctggtctatctccaaagat-----tatgatccgc	106			
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QY	1184	caacgcgttcaacggttaaaattttaaagttgggaaagcaaaatggcggttcaagaactatt	123
Db	1157	CAAAATTAATTCATTAACAAATTTAGAAATGGGAAAAAAATTAATCAGGTAAAGAACTACT	1216
QY	1244	ttgaataaagctatgatcttcgtttatgctgttctttaagcttaacttaaaatttttgt	1303
Db	1217	TTGAAATATGGTTAGCATGCCCGTTATCTTGCGAATTTTACAAGATAATATGAAATTCCTTAC	1276
QY	1304	ctggagcttaataaagatttggaaacttgaagctgtatcttgaatccaataccaacaacgtttgg	1363
Db	1277	TGAACCTTAACAAAGAAATTTACAGCAACACGTCATTCGCTATTATTCACAGCAAGCAATGGG	1336
QY	1364	ataataatcttggtagtttagcaagttatccaattvgggtgaacgcattaaagcgcgaa	1423
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QY	1424	aagcttatgcagatgctcttttgaagatgagcaagaaagttgaagctgtgttccaattactt	1483
Db	1397	AAGCCTATTTGGATGAGCTTTTGAAGAAAGCAACACATTTAAAGCCGATTAATAATTAGTACAGT	1456
QY	1484	ttgagcttaaacctggtatcatatagacattagtaattcaaatgggaaaaaagcgaagcgt	1543
Db	1457	TGGATTTGGCAAAACGGTATTATTGATTTGATGATTAATTGGGTTAAAGCAAAATCTGACATA	1516
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QY	1604	gttaaatccttcttatataaataaattlaaatctggagctgtttaaanaacttggcgaattacg	1663
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QY	1664	atggagagagcttagtcttcaaatagattctctctaagttatcttaagctggttagccgaagacg	1723
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QY	1724	aaggacgaagcggagatttgggtctaattgtaatgcaaaa-----g	1762
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QY	1763	ctggcaatgtagatcttctgttgtgtcaaggtlaaaatgtaattgattggttggagatgac	1822
Db	1757	AAGGTATGACCAACGATTTGTTGGTTTGCTGACGACGGAATTTGAATGGCGGTGAAGGTT	1816
QY	1823	acgatctgtctctctctagtaaaagcggagatttggtaattactgtctgtagtgaagca	1882
Db	1817	ACGACCGAGTTCACTATAG---CCGTGGAACCATATGTGTGCTTAACCTATTGATGCAACA	1873
QY	1883	gtgcaacagaagagcagttatacagtttaactgtaagcttgttcgagtgatatactacc	1942
Db	1874	AAGAGACCGCAAGGTAGTTATACGCTAAATGCTTTCGTAGAAACCGGTAAAGCACTAC	1933
QY	1943	atgaagtttgtgaagcgttcaagaaaccaaggttgggttaacgttactgaatactaccaglatc	2002
Db	1934	ACGAACCTGACTTCACCCATACCGCATTTGTGTGGCAACCGTGAAGAAAAATATGATTAATTC	1993
QY	2003	gttattatgaattaaagaagaagttgggtatggttatacgaagctaccogtaatttgaatcog	2062
Db	1994	GTCATAGCAATTAACGACGCCATG---CCGGTTATTACACCAAGATACCTTTGAAGCTG	2050
QY	2063	tgaagaagaatattgttcttcaattaaatgaatgatttcaaaagtttcaaatccaagaca	2122
Db	2051	TGGAAGAAATTTATCGGTACATCAATTAAGATATCTTTAAAGTAAAGTTCAATGATG	2110
QY	2123	tattccatagttgttgaaggttgatgatttaactcogaatgtgtgtcgttgaagcagcgttgt	2182
Db	2111	CCTTTAACCGTGTGTATGTGTGCAATCAATTTAGCAGGTACGATACGCAACGCAATGACCGCTTAT	2170
QY	2183	ttgtgttgtaagaagcaacgttcgactcttcgggagatgaaagcgatgatttaccogattgagc	2242
Db	2171	TTGGTGTGAAGCCGATGATTTATCTTCGATGTGTGGAAATGGTATGATTTTATTCGATGGCG	2230
QY	2243	gttcctgtgtagatgtagtlatbtaaatgtagtgcgtgaatgtagtctatatacttcttgcgaag	2302

Db 2231 GTAAAGCAACGACCTATATACAGCGTGGCAAGGCGCATGATATTTGCTACCGSTAAG 2290
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Db 2291 GCGATGGTAAATGATATTAACCGATCTGACGCAATGATTAATATCTCTCATAT 2350
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OY 2423 atcatcaggtagtataatcaaccaagatgtaacatacaaatltaacaaa----- 2477
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OY 2478 -----tatacaagtaataaacaagatcataaattgagcaactatgtgtaagaatgta 2533
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Db 2528 AGCGATCACCCTAAAGCAAGTTGATGATCTTAT 2561

RESULT 15
US-07-960-932-8
: Sequence 8, Application US/07960932
: Patent No. 542210
: GENERAL INFORMATION:
: APPLICANT: POTTER, ANDREW A.
: APPLICANT: REDMOND, MARK J.
: APPLICANT: HUGHES, HUM P.A.
: TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ROBERTA L. ROBINSON
: STREET: 635 BRYANT STREET
: CITY: PALO ALTO
: STATE: CALIFORNIA
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk.
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/960,932
: FILING DATE: 19921014
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: ROBINSON, ROBERTA L.
: REGISTRATION NUMBER: 33,208
: REFERENCE/DOCKET NUMBER: 9000-0016, 20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 617-8999
: TELEFAX: (415) 327-3231
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2838 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..2829
: US-07-960-932-8

Query Match 29.3%; Score 814.4; DB 1; Length 2838;
Best Local Similarity 60.2%; Pred. No. 2,9e-177;

Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;
OY 53 caaatcttgatataaanaacttacttgctatcccaaat-----tatatccgc 106
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OY 107 aaaaagtgaggacttaaatgatttataagcttgctgtaataagtaagtaagcttcgct 166
Db 89 AACAGGTAATGCTTTACAGATTTAGTCAAGGCGCCGAAGAGCTGGGATTAAGGTAC 148
OY 167 tagcagaagagcctaactacactgaacagcaaaaaatcgtgtacacagtaaatcagt 226
Db 149 AAAGAGAGAAAGCCAAATATATTTCAACAGCTCAACAGATTGAGCAGATTCAACCG 208
OY 227 ttctctctccacaacactggtatgctatcttctgcaacaaattgaaaagtcttac 286
Db 209 CTATTTGGCTTAACAGACCGTGGCATTTGTTATCTCGCTCCACAAATGATTAATTTGCTAC 268
OY 287 aaaaactctaccaaagtttagcaaaaggttagacagtgtagaataatgatcgta 346
Db 269 AGAAA-----ACTAAAGCAGGCGCAAGCATTTAGTTCTGCGGAAGCATTTGACMAA 319
OY 347 aataggtaaagcaagtaatgtaatacaaatgaagctcttcttgagcaatgtag 406
Db 320 ATGCAAAATTAAGCCAAACGTATATCTGCGATTTCAATCATTTTGGCTCACTATTGG 379
OY 407 cgggtatagaactgtatctttaaataaaaaaggtgatgctgcaactgactgctgta 466
Db 380 CTGGAATGAGATTAGATGAGGCGCTTACGAA--TTAACAGCAACCAACATGCTTCTGCTA 436
OY 467 aagtaagtactgacttgatgaatgagtaattgttaactatctacacagtaactaaaga 526
Db 437 AAGCTGCTTGAGCTTAACAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTA 496
OY 527 ttgaagcatttctcacaagtttagcaagtttagttctacatacgcaggtcaaggtc 586
Db 497 TTGACGAATTTGCTGACCAATATGTCATTTGGTTCAAAACATCAAAATATCAAGGCT 556
OY 587 tctctaataagaagaacagttgcaaaacttaact--tttctaaacaaacttggtc 643
Db 557 TAGGACTTTAGGAGACAACTCAAAAATATCGCTGACCTGATTAAGCTGGCTTGCTT 616
OY 644 tggaaataactgctgttgctacaggaacttctgaggtctgcttgcttgaggaataaa 703
Db 617 TAGATGTTATCTCAGGCTATTAATCGGCGCAACAGCTGCATTTGCTTCAGATATAA 676
OY 704 atgcatcagctgagcaaaaagttgctgaggtttgtaataagaacatgaattatgta 763
Db 677 ATGCTTCAACAGCTAAAAAAGTGGGTGCGGCTTTGAATTGGCAAACTGTTGTTGTA 736
OY 764 atgtaaacaaaagcaattcttcaatglttttagcaacagtggtgctgctgctatcaa 823
Db 737 ATATTACCAAGCCGTTCTTCAATTTTAGCCCAACGGTGGCAGCAGTTATCTT 796
OY 824 ctactggtgctgtgctgcttaacttaactcaatgataatgttggaactgctcttgg 883
Db 797 CAATGGGCGCTGCTGCTGCTTATTTGCTTCTTCTGCGCATTAAGCCATTAAG 856
OY 884 cattatgaatgcaagcaataaaltcaatcagtaatgctgctgagtggttgcaaac 943
Db 857 CATTTGCCGTAATGCGGATTAATTAATCAAGAAAAGTTTAGAGAGTTAGCCCAAC 916
OY 944 aatccgaaaaattgctatgataaggaatcattatgctgtaatacagcggtggtg 1003
Db 917 GCTTTAAAAAATTAAGCTATGACGAGATTAATTAATTAAGCAATTAACAGCGGGAACAG 976
OY 1004 gtactatgagcttcaactaactaactagtagtaagcagtaagtgagcagttctgctggtg 1063
Db 977 GGAATATTGATGCAATCGCTTACTGCAATTAATTAACGCAATTAATTAATTAATTAATTA 1036
OY 1064 ttccgctgctgctgtagatctgctgctgctgctgctgctgctgctgctgctgctgctg 1123
Db 1037 TGCTGCTGCTGCAAGCGGCTGCTTATTTGCTTACCGATGCTTATTAATTAATTAATTAATTA 1096

QY 1124 ttacagattgctctctggaattttagaagcgtctaacagcgcaatgtttagaaagtgtg 1183
 Db 1097 ttacccgggttaattttacgatttctgcaattttcttaaaacgaacgattgtgacacgttg 1156
 QY 1184 ctacacggttctacaggttaaaattttagagtggaagcaaaatgagcggtcgaacattt 1243
 Db 1157 CAAATTAATTCATACAAATTTGTAGATGGGAAAAAATATACCGGTAAAGACTACT 1216
 QY 1244 ttgataaagcgtatgattctcgtttagctgcttatttagactaaactaaattttgt 1303
 Db 1217 TTGAAAAATGTTAGCATCCCGTTATCTTGGCAATTTACAGATATATATGAAATTTCTTAC 1276
 QY 1304 ctgagctaaataaagagttggaagcgtggaagcgttattgcaatcccaaaacagttgg 1363
 Db 1277 TGAATTTTAACAAAGATTACAGGACAGACGTGTCATGCTATTACTACAGCAATGG 1356
 QY 1364 ataataatctggtgagttagcaaggtatctaacaaattggttgaaacycaattaagacgga 1423
 Db 1337 ATTAACAACATTGGTATTAGCTGGTATTAGCCGTTTGTAGTAAAGTCCCTTGTGGTA 1396
 QY 1424 aagcttaagcagatgctttagaagtggaagaaagttgaagcgtggtccaatattactt 1483
 Db 1397 AAGCCTATGTGATCGCTTTGAAAGGCAACACATTAAAGCGATTAATTTACTACAGT 1456
 QY 1484 tggatgctaaacgtgtatcatagacattagtaattcaaatgysaaaaaaacycaagcgt 1543
 Db 1457 TGGATTTCGGCAAAAGGTATTATGATGTGATTAATTCGGGTAAACGAAACTCGACATA 1516
 QY 1544 tgcattcaactcgccttgtttaaagcaaggaacgtgaatcaagttgaagtttaactatg 1603
 Db 1517 TCTTATTCGAACGCCATTATTGACGGCGGACAGACAGCANTGTGACGGTACAAACAG 1576
 QY 1604 gtaataactctataatlaaagttaaatctcgagcgtgtlaaaaaacgtgcaagttacag 1663
 Db 1577 GTAATATATATATTTTACCAAGCTCAATATTACCGTGTAGTACGTGGAATTTACAG 1636
 QY 1664 atgagaagcgtagttcttaaatagatttcttaagttatcagcgtgtgacgagacag 1723
 Db 1637 ATGCTGACACAGTCTTACCTTTGATTAACTTAACGTTGTCAGCGTATTGGTATTGAAT 1696
 QY 1724 aagggcaagaagattgtgtctaatagtaaatgcaaaa-----g 1762
 Db 1697 TAGACATGCTGAAATGTAACCTAAACCAAAAGAAACAAATTTATTCGCAAACTTTGGTG 1756
 QY 1763 ctggcaatgacatatcttctgtgtcaaggtlaaaatgaaatattgattgtgagatgagc 1822
 Db 1757 AAGGTATGACAAAGTATTGTTGTTCTGTACGACGAAATGTGATGGCGTGAAGGTT 1816
 QY 1823 aagatcgtgtctctctataagaaagcagagattgtgtataattactgtatagatgtacga 1882
 Db 1817 ACGACCGAGTTCACATAG---CCGTGGAACACTATGTGCTTTAACTATTGATGCAACCA 1873
 QY 1883 gttgcaagaagaagcagattatagacgttaaatgtaagttgtcgtgagttatctacc 1942
 Db 1874 AAGAGACCGGACAGGTAGTTATACCGTAAATGTTTCGTAGAAACCGGTAAAGCACTAC 1933
 QY 1943 atgaagtttgaagcgtlcaagaacaaggttgggtlaaacgttactgaactatccaglatc 2002
 Db 1934 ACGAATGACTTCAACCCATACCGCAATGTGTGGCAACCGTGAAGAAAAATGAAATATC 1993
 QY 2003 gtgattatgaatlaaagaagttgggtatgtatcagtlctaccgataatttgaatcag 2062
 Db 1994 GTCATGACATTAACCGACACCATG---CCGTTATTACACCAAGATACCTTGAAGCTG 2050
 QY 2063 taagaagaagaattgtttctcaattaaatgattcaaaagttctaaatctcaacagaca 2122
 Db 2051 TTGAAGAAATTAATCGTACTCATCATACGATATCTTTAAAGGTAGTAAGTCAATGATG 2110
 QY 2123 taltcataatgtggaaggtatgattactcgtatgtgtgtgtgacgacgctgtg 2182
 Db 2111 CTTTAACGTTGGTGAATGTTGTGATACATATGTACCGTAAAGCAATGACCGCTTAT 2170

QY 2183 ttgtgtlaaagcaacagatcagacttctggaagatgaagcgatgtactcgtatgctg 2242
 Db 2171 TTGGTGTAAAGCGATGATATTCTCGATGTGGAATGGTATGATTTTATCGATGGCG 2230
 QY 2243 gtctgtgtatgattatlaaagtgtgtgtgtgtgtatgtatgtctatctcgtggaag 2302
 Db 2231 GTAAAGCAACGACCTATTACCGGTGGCAAGGGCGATGATTTTTCGTCACCGTAAG 2290
 QY 2303 gtatgttgaatgacttgtacgattgcaagcggaatgaataatlaagattgtcagatg 2362
 Db 2291 GCGATGATATGATATTATTACCGATTCTGACGCAATGATTAATATCATTTCTCGATT 2350
 QY 2363 caaatatctgatatgattgaacgtaccaaagaggtatctatagttaaagaatg 2422
 Db 2351 GCAACTTAAAGATTTTAACTTTGAAAAAGTTAAACA---TAATCTTGTATCAGCAATA 2407
 QY 2423 atcttcaagttagatttaacatccaaagattggttacataacatacaaatcttaaaaa 2477
 Db 2408 GCAAAAAAGAGAAAGTACCATTTCAAAACTGTTCCGAGAGGCTGATTTGCTAAAGAG 2467
 QY 2478 ----tlatcaaaagtaataaaacagatcataaaattgagcaactaatgtgtaagatgtga 2533
 Db 2468 TGCTTAATTATTAAGCAACTTAAGATGAGAAATCGAAGAAATCATCGTCAAAATGGCG 2527
 QY 2534 gtatatacttccgatacaaatgtataaat 2567
 Db 2528 AGCGATTCACCTCAAGCAAGTGTATGATCTTAT 2561

Search completed: September 15, 2002, 11:17:13
 Job time: 15360 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:56:42 ; Search time 65.81 seconds
(without alignments)
2436.807 Million cell updates/sec

Title: US-09-884-696-2
Perfect score: 4646
Sequence: 1 MSNINVIKSNIOAGLNTSKS.....SSNALQPIPTQGLAPSV 927

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

1: SP_TREMBL_19:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rv1rus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4646	100.0	927	2	093GI2
2	2358.5	50.8	946	2	09EV24
3	2356	50.7	953	2	09EV23
4	2355	50.7	953	2	09EVX2
5	2355	50.7	953	2	09EV25
6	2345	50.5	953	2	09EV26
7	2338.5	50.3	953	2	09EV32
8	2336.5	50.3	953	2	09EV33
9	2332.5	50.2	953	2	09EV28
10	2332	50.2	953	2	09EV25
11	2329.5	50.1	953	2	09EV31
12	2329	50.1	953	2	09EV27
13	2329	50.1	953	2	09EV29
14	2326	50.1	953	2	09EV34
15	2320	49.9	954	2	09EUE1
16	2307	49.7	953	2	09EV30

17	2286	49.2	955	2	09EV22	09ev22 pasteurella
18	2274	48.9	955	2	09EUD4	09ev24 pasteurella
19	2233.5	48.1	956	2	093NP1	093np1 actinobacil
20	2008.5	43.2	1049	2	09RCG8	09rcg8 pasteurella
21	1960.5	42.2	1052	2	093NP0	093np0 actinobacil
22	1820	39.2	1055	2	043892	043892 actinobacil
23	1766	38.0	998	2	085101	085101 escherichia
24	1764	38.0	998	2	09LC58	09lc58 escherichia
25	1760	37.9	998	2	P71223	P71223 escherichia
26	1752	37.7	998	2	046716	046716 escherichia
27	1740	37.5	1022	2	093NP2	093np2 actinobacil
28	1738	37.4	998	2	047461	047461 escherichia
29	1733	37.3	998	2	047262	047262 escherichia
30	803	17.3	1706	2	091469	091469 bordetella
31	482	10.4	233	2	051865	051865 pasteurella
32	411	8.8	1208	16	09PEF19	09pef19 xyella fas
33	410	8.8	1636	16	09PEL7	09pel7 xyella fas
34	391	8.4	2064	16	09PAT8	09pat8 xyella fas
35	383	8.2	208	2	051868	051868 pasteurella
36	367	7.9	850	2	0937V6	0937v6 bordetella
37	365	7.9	697	16	0937V8	0937v8 bordetella
38	365	7.9	850	2	0937V0	0937v0 bordetella
39	364	7.8	850	2	0937W1	0937w1 bordetella
40	364	7.8	850	2	0932Y7	0932y7 bordetella
41	363	7.8	850	2	0937V9	0937v9 bordetella
42	363	7.8	850	2	0937V5	0937v5 bordetella
43	363	7.8	850	2	0937V4	0937v4 bordetella
44	362	7.8	850	2	0937V8	0937v8 bordetella
45	360	7.7	850	2	0937V7	0937v7 bordetella

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	927 AA.
093GI2	093GI2			
AC	093GI2:			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	RTX TOXIN.			
GN	MBXA.			
OS	Moraxella bovis.			
OC	Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.			
OX	NCBI_Taxid=476;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN-TIFTON I;			
RX	MEDLINE=2138402; PubMed=11497442;			
RA	Angelos J.A., Hess J.F., George L.W.;			
RT	"Cloning and characterization of a Moraxella bovis cytotoxin gene.";			
RL	Am. J. Vet. Res. 62:1222-1228(2001).			
DR	EMBL; AF205359; AAK84651.1;			
SO	SEQUENCE 927 AA; 98845 MW; F4B703577E10A96D CRC64;			

Query Match	100.0%;	Score 4646;	DB 2;	Length 927;
Best local Similarity	100.0%;	Pred. No. 7.8e-199;		
Matches 927;	Conservative 0;	Mismatches 0;	Indels 0;	Caps 0;
QY	1	MSNINVIKSNIOAGLNTSKGKRLYLAIKPDYPOKGGTLNDRIKADELGIARLAEPP	60	
DB	1	MSNINVIKSNIOAGLNTSKGKRLYLAIKPDYPOKGGTLNDRIKADELGIARLAEPP	60	
QY	61	NHETAKSVDTVNOQFSLTQTGAISATKLEKFLQKHSNKLAKGLDSVENIDRLGKA	120	
DB	61	NHETAKSVDTVNOQFSLTQTGAISATKLEKFLQKHSNKLAKGLDSVENIDRLGKA	120	
QY	121	SNVLSTSSFLGALACIEIDSLIKKGDAADALAKASIDLINETIGNLSQSTQTLEAFS	180	
DB	121	SNVLSTSSFLGALACIEIDSLIKKGDAADALAKASIDLINETIGNLSQSTQTLEAFS	180	

QY	820	-ITS1L	YOSGNKNDKDHKEOLIKDGDSYTSDDQIDKLQDKKDDGVNITSQELKLADENK	878
DB	838	DPAAEVRNRYKATK	-DEKTEITIGGGERITSKQYDDLL--AKNGKITIDDELSKVVNDE	894
QY	879	SQKISASDIASSLNKLIVGSMALFGTANVSNNALQPIPTQPGI	922	
DB	895	LLKHS-KNVTNSLQKLISASAFITSSNDSNRVLVAFTSMDOSL	937	
RESULT	3			
Q9EV23		PRELIMINARY;	PRF; 953 AA.	
AC	Q9EV23;			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	LEUKOTOXIN.			
GN	LKTA.			
OS	Mannheimia glucosida.			
OC	Bacteria; Proteobacteria; gamma subdivision: Pasteurellaceae;			
OC	Mannheimia.			
OX	NCBI_TaxID=85401;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-PH290;			
RX	MEDLINE=21101823; PubMed=11157953;			
RA	Davies R.L., Whitlam T.S., Selandar R.K.;			
RT	"Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)			
RT	Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)			
RT	haemolytica.";			
RL	J. Bacteriol. 183:1394-1404(2001).			
RJ	EMBL; AF3145422; AAC40306.1;			
DR	InterPro: IPR001753; Enoyl_CoA_hydrtse.			
DR	InterPro: IPR001343; Hemolysn_Ca_bind.			
DR	InterPro: IPR003355; RTX_N.			
DR	Pfam; PF00353; hemolysincabind; 1.			
DR	Pfam; PF02382; RTX; 1.			
DR	PRINTS; PR00313; CANNONGRPT.			
DR	PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.			
SO	SEQUENCE 953 AA; 102150 MW; D99C36DA595B1624 CRC64;			
Query Match	50.7%; Score 2356; DB 2; Length 953;			
Best Local Similarity	49.5%; Pred. No. 5.4e-97;			
Matches	471; Conservative 182; Mismatches 258; Indels 40; Gaps 15;			
QY	1	MSNINV-IKSN---IQADLNST-----KGLKLNLYAIPIKD--YPDQKGTIND	43	
DB	5	LTNISTNKSXSWLPAKSLNRTGOSLAKAGOSLKGAKKIILYIPKDYDTEKNGSLQD	64	
QY	44	FIKADELGIARLEAEPNHTETAKKSDVDVNOFLSLTQTGIAISATKLEKFLQKSTNKL	103	
DB	65	LVKAAEELGIEVQKEGNDIAKQISLTGIQVLTGERTGIYLSAPOLDKLQK---TKV	121	
QY	104	AKGLDVSVDNRDKIGKASNVLSFSSFLGTALAGIELDLSLIRKGDAAADAKASIDLIN	163	
DB	122	GOAISAENLTKRGFSNATVLSIGISILGSLVAGMDLDEALQK-NSNELTLAKAKLELTN	180	
QY	164	EILGLNSTQGTIEFSSQLAKLSTGIQAKGFSNIGKNLQULN-FSKTNLGLLEITIGLL	222	
DB	181	SLIEINANSVTKLDFGGQINDQGLKNVGLSLGKLGKLSGFDRTSLGLDVVSGLL	240	
QY	223	SGISAGFLADKNASTGKRVVAGFELSNQVIGNTKATISSYVLAQRVAAAGLSTGAVAA	282	
DB	241	SGATATVLAADKMASTSKRVGAGFELANQVGNITKAVASSYTLAQRVAAGLSTGPVAA	300	
QY	283	TTSSIMLAISPLAFNMAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQVGTIEASTL	342	
DB	301	IASVSLAISPLAFAGIDKRFNHAKSLESYERFKKLGIDGNDLLAEYQVGTIDASVT	360	
QY	343	TISTATLAVGACVSAANVAGSAGATIALLVAGVTGLISILEASQANFESYANLQKGT	402	
DB	361	AINTALAIAGVGSAAAGSVIASIALIVSGTITVITSTILOYSKQANFEHVAINTHNT	420	

QY	403	LEWENONGGOWPEKQYGRSAALYANNLKFESEKTELEBERVATITPOOHNDNIGELA	40
Db	421	VEEMNNKNNKNTFENGXYDARYLANLQDMKFEFLNLKLEQERVATITPOOHNDNIGELA	48
QY	463	GITTKGERIKSGKAADAFEDDGKKVYACASNITLDAKTIIDISNSNGKQTALHTSPUL	52
Db	481	GISRLEGVLSGKALVYDAFEECKHLKAKIKVLDGANGIIDVNSNGKAKTQHIIIFRTPLL	54
QY	523	TAGTESRERLTNGKYSYINKLKFGKRVKMVYTDGEASSKLDEFKVIQVY-----AETE	57
Db	541	TPTGETHRERIRIQGKXEYITKLININRVDSWKITDGAASSTFDLTINVQIRIGIELDNAGVNT	60
QY	576	GTDDELGLVNNKAGDDLFVGGGKNNIDGSGCHSDVNFVSKOSGPGONTIVDGSATEAGSY	63
Db	601	KTKERKIVAKLGAGDDNVFVSGSTTEIDGSEGYDVHYSR-GNYALATYIDAKKETEGOGSY	65
QY	636	TVNRKRVARGDLYHEVYVKKOETKVGKRTETIOYRDYELKRVGYXGYSTNLKSVEEVISOQ	69
Db	660	TVNRREVVEGKALHETVSTHTALVGNREKIEYR-HSNQNHAGYTTKPTKLAVEELIGTS	71
QY	696	FNDVFKSGKFNDIFHSGEGDLDLGGAGDDRLFGKGNDRLSGDEGDDLLDGGSGDDVYN	75
Db	719	-HNDIFKSGKFNDAFNGGSDGVLTIDGNDGNDRFLFGKGCDDIIDGGNGDGFIDGKGNDDLH	77
QY	756	GGAGNDVYIFPRKSGNDPLTLYOGSTGNDKLAADANISDIIMEIKTKEGIIVKRRDHSGINI	81
Db	779	GKGDDIFVHRGGDDNITITDSDGDKSFSNSLKLDFEEVYKHNLYV-TSKREKVTI	83
QY	816	PRWY----ITSNLQVYQSKTDDHKLEOLIGKSGSYTSPQIDKILQDKKDGTVITSOELK	87
Db	838	QDMFEADPAKRVNRYKATK-DEKIEIILIGGGERITSKQVDDL-AKNGCKITODELS	89
QY	872	KLADENKSKOKLSASDIASLKLKLVSMALFGTANSVSSNALOPTIQQPYGI	922
Db	895	KVVDVYELLKHS-KNVTNSLDKLISSASAFITSSNDSRNVLVAPMTMDQSL	944
RESULT 4			
Q9ETX2			
ID	Q9ETX2	PRELIMINARY: PRT: 953 AA.	
AC	Q9ETX2:		
DT	01-MAR-2001 (TREMblrel. 16, Created)		
DT	01-MAR-2001 (TREMblrel. 16, Last sequence update)		
DT	01-JUN-2001 (TREMblrel. 17, Last annotation update)		
DE	LEUKOTOXIN.		
GN	LKTA.		
OS	Mannheimia glucosida.		
OS	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;		
CC	Mannheimia.		
OX	NCBI_TaxID=85401;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=PH498, AND PH344;		
RA	Davies R.L., Whittam T.S., Selander R.K.;		
RT	"Sequence diversity and molecular evolution of the leukotoxin (lktA) gene in bovine and ovine strains of Mannheimia (Pasteurella) haemolytica."		
RL	J. Bacteriol. 0:0-0(2001).		
EMBL	AF314518; AAC40302.1; -		
DR	EMBL; AF314517; AAG40301.1; -		
DR	InterPro: IPR001473; Emoyl_CoA_hydrtase.		
DR	InterPro: IPR001433; Hemilyn_Ca_bind.		
DR	InterPro: IPR003355; RTX_N		
DR	Pfam: PF00353; hemolysinCbind. 1.		
DR	Pfam; PF02382; RTX; 1.		
DR	PRINTS; PR00313; CABNDNGRPT.		
DR	PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.		
SEQ	SEQUENCE 953 AA; 102135 MW; 70DB354157F5881E CRC64;		
Query Match 50.7%; Score 2355; DB 2; Length 953;			
Best Local Similarity 49.5%; Pred. No. 6e-97;			

	Matches	471; Conservative	182; Mismatches	256; Indels	40; Gaps	15;
OY	1	MSNINV-IKSN--IQAGINST-----KSLKLNLYLAIPKD--YDPQKGTIIND	43			
Db	5	LNFTSTNLKSMWLTAKSGSNLRTGQSLAKAGQSLKGTAKKILLYIPKDYDPEKNGIQQD	64			
OY	44	FIKADELGIARLAEPNPTETAKKSVDTVNPFLSLPQTGLAISATKLEKELKSTNKL	103			
Db	65	LKKAABEELIEVOKERGNIDAKAQSTSLGTIQVNLGLTERGIVLASAPOLDKLQK--TPV	121			
OY	104	AKGLDSEVNIIDRKLKGSAAVVLSTLSEFLGATLALGIELSLIKGAAPDALAKASIDILN	163			
Db	122	GQAISGAENULTGFSNAKTVLSGIOSILDSYLAGMDLDAQK--NSNELTLAKAGLETLN	180			
OY	164	ELIQLNSQSTQTLIEFSSQALKGSTISQAKGFSNIGKLNQIN--FSKTNLGLTITGL	222			
Db	181	SLIENIANSVKTLLDAFDQDINQSGKLNQWKLSSIGDKTKLGSDPKDTSLGLDVSGL	240			
OY	223	SGISAGFALADNASTGKKVVAAGFELSNOYIGNVIKAISSYVLAQRYAAGLSTGAVAA	282			
Db	241	SSATTAALVADNASTSRVAGFELANOVGNITKVAVSSYLLAQRVAAGLSTGPVAA	300			
OY	283	ITSSIMLAIPLAFMAADKFNHANAIDFEAFQFRFGDGDHLLAEVORGSTIEAST	342			
Db	301	IASYSLAISPLAFAGIADKFNHANSLESTAAFRPKLGTGDNLAETORGSTIDASVT	360			
OY	343	TSTALGAVSAGVSAAAVSAVGAFLALVAGVTGLISGIELASKQAMFEVANKLOGKI	402			
Db	361	AINTALAAIAGVSAASAAAGSVIAPLALLVSGITGVISIIQYSGQAMEHVAHNKHI	420			
OY	403	LEMEQNGQANTFDKGYDSRYAATYLAANNIKELSELKELEAERYALITQORMANNIGELA	462			
Db	421	VEMEKNNHKNFENGYSARYALANIQDNMKFLNLINKELQAEARYALITQOQDNINIGDLA	480			
OY	463	GJTITGERIKSGKAAVADPEDEGKYAGSNIILDKGTGIIISNSNGKQTAALHTSPLL	522			
Db	481	GISRLGEKLSKRAYADAEESGHLKADKLYOLDSDANGIIDSNSGAKTQAHILFRPPL	540			
OY	523	TGATESRERLTNGKXSYINKLKEFGVKMWQVYDGEASSKLDPSKYTORV-----AETE	575			
Db	541	TPGTEHREVRVQGYKEYITKLININRVDSMKITDGAASSFPDLTVNVQRIEILDAGAVT	600			
OY	576	GIDELIGLYNAKAGNDLIFVGOGKANNIDGGCHDHFVYSKDGFGCNITVDTSATAGSY	635			
Db	601	KTKERKIVAKLAGADDNVEFGSTTEIDGEGEDYDVHYSR--GNYGALMIDATKETEQGSY	659			
OY	636	TYNRRVARDIIVHEVVKRQETKVGKRTETIOYRDVLEKRVGQGYOSTNKSVEERTISQ	695			
Db	660	TYNRRVEVGKALHEVTSYHTLALVGNREEITERY--HSNNQHNAGYTTKTLAAVEEITGTS	718			
OY	696	FNDVERGSKFNDIFPSGEGDDLLDAGAGDDRLFEGKAGNDRLSGDGDDBLLDQSGSDVJLN	755			
Db	719	HNIDIFKSGKFNDAFNGDQDVPTIDGNDGNDLFGGKGGDDIIDGNGDGFIDSGKKNDLH	778			
OY	756	GGAGADVITFFRGDGDNDLTYDGTGDKLAFADANISDIIMEFTKGCITLYKRNHSGSINI	815			
Db	779	GKGGDIDIFVHRGDDNDIITDSDGNDKLSFSSNSNLKDLTFEKKVHNLYI--TNSRREKTYI	837			
OY	816	PRWY-----ITSNLQVYOSKTKDKHLEOLIKGQSVITSDQIDKLIQDKKDGIVTISQELK	871			
Db	838	QDMFEADPAKVVRYKATK--DEKTEETIIOGERTISQYQVDDL--AKNGCKITQDELS	894			
OY	872	KLADENKSOGLSASDIASLKLNVKLSMALLFGANSVSSNAQLOPIPTQPGI	922			
Db	895	KVVDVYELLKHS--KNVTNSLDKLSISASAFISSNSNRVAVLAFTSMIDQSL	944			
RESULT	5					
ID	09EV25					
NC	09EV25	PRELIMINARY;	PRT:	953 AA.		
DT	01-MAR-2001	(TREMBLrel. 16, Created)				
DT	01-MAR-2001	(TREMBLrel. 16, last sequence update)				

Query Match	Best Local Similarity	Score	DB 2	Length	953
Matches	471: Conservative	182:	Mismatches	258:	Indels
					Gaps
1 MSNINW-IKSN--IOAGINST-----KSGLNLYLAIPKD--YDPQKGGTLND	43				
5 LFNISTNLKSSMLTKSGNRTGQSLAAGSLKTKGAKIILYIKXDYDTEKNGGLD	64				
44 PIKADELGIARLAEPNHTETAKRSVDTVNQLSTOTGIAISATKLEKFLKHSTNKL	103				
65 IVKAAEEGLIEVQKEEGNDIAKQTSLGITQVNLGTERGIYLSAPQDLKLQK--TKV	121				
104 AKGDQSVENIDPKLQKASVNLSTLSEFLGTALAGIELDSLIRKGAAPDALAKASIDLIN	163				
122 GQAISSAEELTKGFESNATVILSGISLISGLVAGMDLDEALQK--NSNETLTAKAGLELTN	180				
164 ELTGNLSOSTQTEAFSSQLAKLGSITISQAKFGFSGNKLQMLN-FSKTNLGLTETGL	222				
181 SLTENIANSVKTLDAFGQINGLSKLQNVKGLSSLGKIKGLSGFDKTSIGLDVYSGLL	240				
223 SCISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISVYLAQVAAGLSTGVAVAL	282				
241 SCATATVILADKNASTSRKVGAFELANQVGNITRKAVSYLLAQVAAGLSTGPAVAL	300				
283 ITTSMILAIISPLAFNMADKFNHANADELFAKQKFPYDGGHLLIAEYORGVTIEAST	342				
301 IASTVSLAISPLAFGIADKRFNHAASLESYERFKKLLDGGNLLIAEYORGVTIDASVT	360				
343 TITSTALGAVSAGVSAAGVAPGIALVLAVGVTLLGISILEASQKAMFESVYANLQKTI	402				
361 AINTLALAIAGVSAAGVAPGIALVLAVGVTLLGISILEASQKAMFESVYANLQKTI	420				
403 LEWEKONGQNTYEDKGYDSRYAAYLAANLKFELSELNKELEAEVRIATITQQRWNNIGFIA	462				
421 VEWEMKNNKNGKVFYEGYDARYLANLDQNMKFLTNLKELOAEVRIATITQQRWNNIGFIA	480				
463 GITTKGERIKSKKATADAFEDGKKVYEAASNTTLDKATGIIDISNSNGKKTQALHTTSP	522				
481 GISIRGEIVYSGKAAVADAFEDGKKVYEAASNTTLDKATGIIDISNSNGKKTQALHTTSP	540				
523 TAGTSESRRLTNGKSYINKLKFQGVKKMOWYTVDEASSKLDPFSKYTOV-----APTE	575				
541 TPGTHREHREVOTGKTEYITTKLININVDGSKITTDGAASSTFDLTINVOIKIGIELDNAGV	600				
576 GTDEIGLLVNAKNDIIFVQGGKNNIDGCGDHRAVFAVSKDGGFNGNITVDGTSATAGASY	635				

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Db 601 KTKETIKVAKLAGADDNFEVSGCTEIDGEGYDRVHYSR-GNYGALTIIDATKETEGSQ 659
QY 636 TVNRKARADIIHEVYKROETKYGKRTETIYQRYDIELRKVGYGYOSTDNKLSVEEYGSQ 695
Db 660 TVNRFETKALHEVSTHTALAGNREEKIEYR-HSNNOHAGYTRYKDTLKAEEIIGTS 718
QY 696 FNDVFGSKFNDIFHSGEDDLIDGAGDDRLFGKGNDRLSGDEBDDLLDGGSGDVLN 755
Db 719 HNDIFGSKFNDAFNAGDDVDITDGDNDRLFGKGGDDIIDGNDDDPFDGSGKNDLH 778
QY 756 GGAGNDVYIFRKGDNDTLYDGTGNDKLAFPADANISDIMEIERTKEGIIYKRNHSGSINT 815
Db 779 GGGKDDIEFVHRQGDNDIITDSGNDKLSFSDSNLKDLPFEKYNHLYI-TNSKREKVTI 837
QY 816 PRMY-----ITSNLYQNSKKTDEKIEQLGKDGSYTTSQIDKIIDKDKDGYITTSQELK 871
Db 838 QDMFREADFAKEVRNRYKARK-DEKIEIIGQNGERTSKOYDOLI--ANGNGKITODELS 894
QY 872 KLADERKSQKLSASDIASSLNKLGVSMALFGTANYSVSNALOPITPOGII 922
Db 895 KYVDNVELLAKHS-KNYTNSLIDKLISASAFSTSSNDSRNVLVAFPSMLDOSL 944

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RESULT 6
Q9EV26 PRELIMINARY: PRT: 953 AA.
AC Q9EV26:
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OS Mannheimia glucosida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=85401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PH240;
RX MEDLINE-21101823; PubMed-11157953;
RA Davies R.L., Whitlam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica."
RT J. Bacteriol. 183:1394-1404(2001).
DR EMBL: AF314519; AAG40303.1.-;
DR InterPro: IPR001753; Enoyl_COA_hydrtse.
DR InterPro: IPR001343; Hemolysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX_1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
SQ SEQUENCE 953 AA; 102236 MW; AC5874B3B75D1C98 CRC64;

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Query Match 50.5%; Score 2345; DB 2; Length 953;
 Best Local Similarity 48.9%; Pred. No. 1.7e-96;
 Matches 468; Conservative 186; Mismatches 250; Indels 54; Gaps 16;

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QY 1 MSNINV-IKSN---IOAGINST-----KSGLKNLYLAIPKD--YDPQKGSTIND 43
Db 5 LTNISTNLKSSWLTAKSGLNRTGQSLAKAGQSLTKGAKKILILIPKDYQDTEKNGGLD 64
QY 44 FTKADELGIARLAEPNHTETAKKSVDPVNOFLSTQTAISARLKEFLQKHSSTNKL 103
Db 65 LVKAARELGI EYQKEEGNDIAKAQISTLTGIIQNVLTGLTBERGIVLSAQQDKLQK---TKV 121
QY 104 AGGLDSVENIDRKLKASAVNLSTLSFGLTALAGIELDSLILKGGDAAPDALAKASIDLIN 163
Db 122 GGAISAEMLITKGFNSAKNLTGSLGSIOSIVLSGLMDLDELAK--NSNETLAKAGLELTN 180
QY 164 EIIIGNLSQSTQRTIENRSSQLAKGISTISQAKGFSNIGNKLQNLN-PSKTNLGLLEITIGLL 222

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Db 181 SLENIANSKVTIDAFGDDQINQSGKLNQNGKGLSSLDKLAGSGDKTSGLGDVYSGLL 240
QY 223 SGISAGFALADKNASTGKKVYAAGFELSNOYIGNVTKAISSYVLAQRYAAGLSTTGAVAL 282
Db 241 SGATLALIVLADKNASTRKYGAGFELANQVGNITRAVSSYIIAQRVAAAGLSTGPVAL 300
QY 283 ITSSIMLATSPLAFMNAADKFNANALDEFARPKFRFGYGDHLLAEYQGVGTIASLT 342
Db 301 IASTVSLAISPLAFAGIADFNHAKSLSEYAEFRKRLGVDGMLAEYQGVGTIASVT 360
QY 343 TISTAGAVSAGVSAAGVAVGAPALALVAGTGLISGLILEASKOAFESVANRLQGI 402
Db 361 AINTALALAGVSAAAGVAVSPALALVSGITGVISTLIQSKQAFEHVANKIHNKI 420
QY 403 LEWEKONGVYFDKQIDSKRYAAYLANNLKELSELNKELEAEVYIAITQQRWNNIGELA 462
Db 421 VEMEKNNHGNYPENGYDARYLANLDNMKFLNLNLKELQAEHYIAITQQRWNNIGDLA 480
QY 463 GTRKLEGRKSKRAYADAFEDGKKVEAGSNITIDAKTGIIIDISNSNKKQALHTSPIL 522
Db 481 GISRLGEKYLISKAYVDAFEEGKHLKADKLVDLSANGIIVDSNGAKTOHILFTRPL 540
QY 523 TACTESRRLTNGKYSYINKLKFGRVKNMOVTDGEASSKIDFSGKIORY-----AETE 575
Db 541 TPTGTEHREKRYQTKYEITITKLNINRVDKMTITDGAASSTDTDLINVOIGIELDNAGNT 600
QY 576 GTDEIGLIVNAKAGNDIEVYGQKMINDGDDHDFVYSKDGFGNTVDGTATAGSY 635
Db 601 KTKETIKVAKLAGADDNFEVSGCTEIDGEGYDRVHYSR-GNYGALTIIDATKETEGSY 659
QY 636 TVNRKARADIIHEVYKROETKYGKRTETIYQRYDIELRKVGYGYOSTDNKLSVEEYGSQ 695
Db 660 TVNRFETKALHEVSTHTALAGNREEKIEYR-HSNNOHAGYTRYKDTLKAEEIIGTS 718
QY 696 FNDVFGSKFNDIFHSGEDDLIDGAGDDRLFGKGNDRLSGDEBDDLLDGGSGDVLN 755
Db 719 HNDIFGSKFNDAFNAGDDVDITDGDNDRLFGKGGDDIIDGNDGDFIDGSGKNDLH 778
QY 756 GGAGNDVYIFRKGDNDTLYDGTGNDKLAFPADANISDIMEIERTKEGIIYKRNHSGSINT 815
Db 779 GGGKDDIEFVHRQGDNDIITDSGNDKLSFSDSNLKDLPFEKYNHLYI-TNSKREKVTI 837
QY 816 PRMY-----ITSNLYQNSKKTDEKIEQLGKDGSYTTSQIDKIIDKDKDGYITTSQELK 871
Db 838 QDMFREADFAKEVRNRYKARK-DEKIEIIGQNGERTSKOYDOLI--ANGNGKITODELS 894
QY 872 KLADERKSQKLSASDIASSLNKLGVSMALFGTANYSVSNALOPITPOGII 922
Db 897 VQNYVELLK-----HSKNYTNLSIDKLISASAFSTSSNDSRNVLVAFPSMLDOSL 944

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RESULT 7
Q9EV32 PRELIMINARY: PRT: 953 AA.
AC Q9EV32:
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PH706;
RX MEDLINE-21101823; PubMed-11157953;
RA Davies R.L., Whitlam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica."

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RL J. Bacteriol. 183:1394-1404(2001).
DR EMBL: AF314509; AAC40293.1; -.
DR InterPro: IPR001753; Enoyl_CoA_hydrtse.
DR InterPro: IPR001343; HemLysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
SQ SEQUENCE 953 AA; 102078 MW; EF425243C8741EE4 CRC64;

Query Match 50.3%; Score 2338.5; DB 2; Length 953;
Best Local Similarity 49.5%; Pred. No. 3.2e-96;
Matches 473; Conservative 183; Mismatches 255; Indels 45; Gaps 18;

QY 1 MSNIN- IKS- --IQAGLST-----KSGIKNLVLAIPKD--YDPQKGTIND 43
DB 5 LTNISTMLKSSMLTAKSGLNTGSLAKAGOSLTKGAKKILLYPKDYQYDTEKGNGLD 64
QY 44 FIRKADELGIARLAEEPNHETAKSVDTVNOFLSTOTGIAISATKLEKFLQKSTNKL 103
DB 65 LVKAAQELGIEVQKEBNDIAKADTSIGTIONVGLTERGIVLSAPOLDKLLQK---TKV 121
QY 104 AKGLDSEVNIIDRLKGSANVLSLSTSLFGLTALAGIELDSLKKGAADALAKASIDLIN 163
DB 122 GOAIGSAENLTKGFSNKTATVLSGIQISLGLVLAQMDLEALQK--NSNELTLAKGLELTN 180
QY 164 EITNLSOSIOTIFAFSSQLAKGSTISQAKGFSNIGNKLOLN--FSKTNLGLIITGL 222
DB 181 SLININANSVTITDAFDQINQGLSKLONVKGLSLDRLKGLSGFDTSLGLDVGSL 240
QY 223 SGISAGFALADKNASTGKVAAGFELSNOVIGNYTKAISSVLAQRYAAGLSTGAAVAL 282
DB 241 SGATPAVLADKNASTSKVAGFELANOVGNITKAVSSITLQRYAAGLSTGPAVAL 300
QY 283 ITSSIMLAISPLAFMAADKFNHANALDEFKQPRKFGYDGDHLLAEYQKGVITTEASLT 342
DB 301 IASTVSLAISPLAFAGIADKFNHAKSLESYAEKFKLGDNDNLAEYQRTGTIDASVT 360
QY 343 TISTALGAVSAGVSAANVSAVAPIALVAGVGLTISGLEASQAFESVANRLQKI 402
DB 361 AINTALAIAGVSAAGVSAVAPIALVAGVGLTISGLEASQAFESVANRLQKI 420
QY 403 LEMEKONGGVYFDKGYDSRYAAYLANNLKFLSELNKLLEAERYAIATQORMDNNGIGLA 462
DB 421 VEMENNGSKNVPFENGQYARLANLQDMKFLNLNKLQAEVYAIATQOOWDSNIGDLA 480
QY 463 GITKIGERIKSGKAYADAFEDGKKVEAGSNTIDAKTGIIDISNGKKGQALHFTSPL 522
DB 481 GISRLGEVYLSGKAYVDAFEEOGHLKADKLVOLDKAGIIDVSNNGEAKTQHILERTPL 540
QY 523 TAGTESRRLTFNGKYSYINKLFGKRVKMWQVYDGEASSKDLFSKVIOHV-----AETE 575
DB 541 TPGTETKRRVQKKEYEITKLHINVDKMTIDGAASPFLDINVQRIEGLDNAGVNT 600
QY 576 GTDEIGLVNAKAGNDLIFVQGGKMNIDGCGHDVRFYSKDGPEGNITVDGSAIEASY 635
DB 601 KIKETKILAKLEGGDNDVFGSGTETIDGEGEDYDRVHSR--GNYGALTIDAKRETEGYS 659
QY 636 TVNRKRVARDIYHEVYKQETKVKRTEFIQYRDYELKRVGYSQSTNLKVEEVIASQ 695
DB 660 TVNRKRVARDIYHEVYKQETKVKRTEFIQYRDYELKRVGYSQSTNLKVEEVIASQ 718
QY 696 FNDVKGSKFENDIFHSGEGDLDLDGAGDDRLFGKRGNDRLSGDEGDLDDGSGDDVYN 755
DB 719 HNDIRKGSFNDAFNGGQVDFTIDGNDRLFGKGGDDIIDGNGDDPFDGKGNDDLLH 778
QY 756 GAGANDVYIFKRGDNDLFDGTGDKLAFADANISDMIEETKKECIYKRNDHSGSINI 815
DB 779 GSKGDDIEFHROGDNDSTIESEGNKLSFSDSNLKLDFEYVNHHLVLT--TFTKQEKYTI 837
QY 816 PKWY----ITSNLQNVQSKTKHKEIQLGKDGSYTTSQIDKILQDKKDGIVTISOELK 871

DB 838 QWFFRAEFKTIQNVYATR-DDKITEIILGONGERTSQQVELIE--KGNGKIAQSELT 894
QY 872 KLADENKSKOKLASNDIASSLNTKLVGSMALFGTANVSSNALDPIQPGGIIAPSV 927
DB 895 KVVNDYQLLKYS-RDASNSLDKLISASAFSTSSD-SRNVL--ASPT-SMDPLSL 944

RESULT 8
O9EV33
ID O9EV33 PRELIMINARY; PRT; 953 AA.

AC O9EV33; 01-MAR-2001 (TREMELREL. 16, Created)
DT 01-MAR-2001 (TREMELREL. 16, Last sequence update)
DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxId=75985;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=PH66.
RX MEDLINE=21101823; PubMed=11157953;
RA Davies R.L., Whittam T.S., Selaender R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and ovine strains of Mannheimia (Pasteurella)
RT haemolytica."
RL J. Bacteriol. 183:1394-1404(2001).
DR EMBL: AF314508; AAC40292.1; -.
DR InterPro: IPR001753; Enoyl_CoA_hydrtse.
DR InterPro: IPR001343; HemLysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
SQ SEQUENCE 953 AA; 102132 MW; 4138AB5FAE2843B3 CRC64;

Query Match 50.3%; Score 2336.5; DB 2; Length 953;
Best Local Similarity 49.6%; Pred. No. 4e-96;
Matches 474; Conservative 181; Mismatches 256; Indels 45; Gaps 18;

QY 1 MSNIN- IKS- --IQAGLST-----KSGIKNLVLAIPKD--YDPQKGTIND 43
DB 5 LTNISTMLKSSMLTAKSGLNTGSLAKAGOSLTKGAKKILLYPKDYQYDTEKGNGLD 64
QY 44 FIRKADELGIARLAEEPNHETAKSVDTVNOFLSTOTGIAISATKLEKFLQKSTNKL 103
DB 65 LVKAAQELGIEVQKEBNDIAKADTSIGTIONVGLTERGIVLSAPOLDKLLQK---TKV 121
QY 104 AKGLDSEVNIIDRLKGSANVLSLSTSLFGLTALAGIELDSLKKGAADALAKASIDLIN 163
DB 122 GOAIGSAENLTKGFSNKTATVLSGIQISLGLVLAQMDLEALQK--NSNELTLAKGLELTN 180
QY 164 EITNLSOSIOTIFAFSSQLAKGSTISQAKGFSNIGNKLOLN--FSKTNLGLIITGL 222
DB 181 SLININANSVTITDAFDQINQGLSKLONVKGLSLDRLKGLSGFDTSLGLDVGSL 240
QY 223 SGISAGFALADKNASTGKVAAGFELSNOVIGNYTKAISSVLAQRYAAGLSTGAAVAL 282
DB 241 SGATPAVLADKNASTSKVAGFELANOVGNITKAVSSITLQRYAAGLSTGPAVAL 300
QY 283 ITSSIMLAISPLAFMAADKFNHANALDEFKQPRKFGYDGDHLLAEYQKGVITTEASLT 342
DB 301 IASTVSLAISPLAFAGIADKFNHAKSLESYAEKFKLGDNDNLAEYQRTGTIDASVT 360
QY 343 TISTALGAVSAGVSAANVSAVAPIALVAGVGLTISGLEASQAFESVANRLQKI 402
DB 361 AINTALAIAGVSAAGVSAVAPIALVAGVGLTISGLEASQAFESVANRLQKI 420


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RESULT 10
O9ETG5 ID O9ETG5 PRELIMINARY; PRT: 953 AA.
AC O9ETG5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OC Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_Taxid=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PH284, PH388, AND PH8;
RA Davies R.L., Whittam T.S., Selaender R.K.;
RT "Sequence diversity and molecular evolution of the leukotoxin (lktA)
RT gene in bovine and ovine strains of Mannheimia (Pasteurella)
RT haemolytica.";
RL J. Bacteriol. 0.0-0(2001).
DR EMBL; AF314507; AAC40291.1; -
DR EMBL; AF314504; AAC40288.1; -
DR EMBL; AF314506; AAC40290.1; -
DR InterPro: IPR001753; Enoyl_CoA_hydrtse.
DR InterPro: IPR001343; Hemolysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS; PR00313; CABNDNGRPT.
DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 101997 MW; D593D6A577C3ADE9 CRC64;

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Query Match 50.2%; Score 2332; DB 2; Length 953;
Best Local Similarity 50.1%; Pred. No. 6.3e-96;
Matches 465; Conservative 175; Mismatches 263; Indels 26; Gaps 13;

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OY 8 KSNTOAGINSTKSGKNTLYAIIPKD--YDPOKGGTLNDFIKADELGARLAEEPHHET 65
DB 28 QSLTDAG--SLKGTAKKIIILYIPQYDTDEQNGLODIVRAAEGLIEVQEEHNNIAT 86
OY 66 AKKSVDTVNOPLSLTGTGIAISATRIEFLQKSTNKLAKGLDSVENIDRLKGNANVL 125
DB 87 AQTSLGTIQTAFGLTERGIVLASPIDIKLQK--TKAGQALGSAESIYONAKKATVLS 143
OY 126 TLISFLGTALAGTIELDSLTKGDAAAPDALAKASIDILMEIIGNSQSTQITAFESSQLAK 185
DB 144 GIQSTILGSLAGMDLDEAL-QNNSQHALAKAGLELTNSLENIANSVKTIDDEFGEQISQ 202
OY 186 LGSTTSQAKGFSNIGNKTONL-NFSKTNLGEITGLSGISAGFALADKNASTKKNVAA 244
DB 203 FEGSKLQNTKGLCTLDGDKLKNIGLDKAGIGLDIVISGLSGAALALVLADKNASTKKNVGA 262
OY 245 GPELSNOYIGNVTKAISSVYLAQRYAAGLSTTGAVAAALITSSIMALISPLAFMNAADKN 304
DB 263 GPELANOYVGNITTKAVSVYLAQRYAAGLSTTGAVAAALITSSIMALISPLAFMNAADKN 322
OY 305 HANALDEFAPKFRKFGYDGDHLLAEYQKVGITEASLTITISALCAVSAAGVAAVGSAY 364
DB 323 HAKSLESYAEFRKFLGYSDDNLAEYQKVGITEASLTITISALCAVSAAGVAAVGSAY 382
OY 365 GAPTLLVAGVTGLISGLEASKQAMFESVANRLQGTILEMKONGGONYPFKGYDSRA 424
DB 383 ASPILALVGLTGVISTILQYSKQAMFESVANRLQGTILEMKONGGONYPFKGYDSRA 442
OY 425 AYIANLKFELSELNKELEAEVYATITQORWNNIGELAGITLGRISKGAADAFEDG 484
DB 443 ANLQNNMKFLNLNKELEAEVYATITQORWNNIGELAGITLGRISKGAADAFEDG 502
OY 465 KVEVGSNTTLDKAGTIDISNSNGKTOALHFTSPLTLAGTESRRLTNGKYSTINKLK 544

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DB 503 KHIRAKDLVOLDSSANGIIDSNSNGKAKTOHILFETPLLTGTEHREVRQYQKEYEITKLN 562
OY 545 FGRYKNNQVTDGESSKLDISKVIORY-----AETEGDELGLYNNAKAGNDIPVGQ 597
DB 563 INRVDSMKITDGAASFEDLITNVVORIGIELDNNAGNVTKEKTKIATLCEGDNNFVGS 622
OY 598 GKMIIDCGDGHDRVYFSKDGFCGNITVDGTSAEAGSYVNRKVARGDIVHEVYKROETK 657
DB 623 GTTEIDGEGEDRHYNR-GNYGALTIDATKEFDQGSYVNRFEVETGKALHEVTSHTAL 681
OY 658 VGRTEITQYRDYELRKVGQYSTDLKSYEYIGSQFNDVYKSGFNDLIFHSGEDDL 717
DB 682 VGNREEKIEYR-HSNNOHHAGYYTKDLKAVEELIGSHNDIRKSGSFNDFNGSDVDY 740
OY 718 LDGAGDRLFGGKGNRLSGEGDDLLDGGSGDVLNAGANDVYIFRRKGNDTLTYDG 777
DB 741 IDGNDGNDRLFGGKGGDILLDGGNDDEFLDGGKNDLHGGKDDIFVHRGDDNDITDS 800
OY 778 TGNDKLAEPADANISDIEMERTKEGIIYVRNDHSGSINIPRWY---ITSNLQYQSKTD 833
DB 801 DGNDKLSFSDSNLKDITFEKYNHLYI-TNSKREKVTIDWFREADPAKEVPYKATK-D 858
OY 834 HKIQILGKDSYTTSDQIDKILQDKDGYITTSQELKLADENKSKLASDIASSLNK 893
DB 859 ERKEIITIGQNERITRSQVDDLI-AKNGKKITQDELKSVYDNYELLKHS-KVNTSLDK 915
OY 894 LVGSMALFETANSVSSNALOPITQTOGI 922
DB 916 LISSVAFSTSSNDSRNVLVAFSTMLDOSL 944

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RESULT 11
O9EV31 ID O9EV31 PRELIMINARY; PRT: 953 AA.
AC O9EV31;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OC Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_Taxid=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PH588;
RA MEDLINE=21101823; PubMed=11157953;
RA Davies R.L., Whittam T.S., Selaender R.K.;
RT "Sequence Diversity and Molecular Evolution of the leukotoxin (lktA)
RT gene in bovine and ovine strains of Mannheimia (Pasteurella)
RT haemolytica.";
RL J. Bacteriol. 183:1394-1404(2001).
DR EMBL; AF314510; AAC40294.1; -
DR InterPro: IPR001753; Enoyl_CoA_hydrtse.
DR InterPro: IPR001343; Hemolysn_Ca_bind.
DR Pfam: PF00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS; PR00313; CABNDNGRPT.
DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102160 MW; A189BF80754A7907 CRC64;

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Query Match 50.1%; Score 2329.5; DB 2; Length 953;
Best Local Similarity 50.1%; Pred. No. 8.1e-96;
Matches 469; Conservative 178; Mismatches 259; Indels 31; Gaps 16;
OY 5 NVKSNIOAGINSTKSGKNTLYAIIPKD--YDPOKGGTLNDFIKADELGARLAEEPHNH 62
DB 25 NAGQSLAKAG-QSLKGTAKKIIILYIPKDYDTDEKNGLODIVRAAEGLIEVQEEGEND 83

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QY	636	FNDVFKSGKFNDFHSEGGDILLDGGAGDRLTGKKNKNDPLSDDEGGDILLDGGSSGDDVYN	753
Db	719	HNDFIKSGKFNDAENGDDVFTIDGNDGNRLFEFGKGGDILLDGGNDDFIDGKGNDLH	778
QY	756	GGACNDVYIFPKGGNDPLVDGTGNDKLAFAADANIDIMIERTEKGIIVRNHSGSINI	815
Db	779	GKKDDILFVHGGGNGDSITESBENKDLSTSDSLKDLFEKYNVHHLVLTNKGKEXVTI	837
QY	816	PRWY----TTSNLNYSNKTDRKIEOLIGKDGSIYITSDDIKLQDKKDGVIYITSOELK	871
Db	838	QNMREAEFAKTIQNYVATR-DDKIEELIGONGERITSKOVDELIE--KNGKIAOSELT	894
QY	872	KLAENKSOKIASADIASLUNKLIVGSMALGETASVSNNLQPTOPTGGILPSPV	927
Db	895	KVDNYQLKTS-RDASNSLDKLSSASAFSTSS--SRNVL--ASPT-SMLDPSL	944
RESULT	13		
Q9EVZ9			
ID	Q9EVZ9	PRELIMINARY;	PRT; 953 AA.
AC	Q9EVZ9;		
DT	01-MAR-2001	(TREMBLrel, 16, Created)	
DT	01-MAR-2001	(TREMBLrel, 16, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel, 19, Last annotation update)	
DE	LEUKOTOXIN.		
GN	LKTA.		
OS	Pasteurella haemolytica.		
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;		
OC	Mannheimia.		
OX	NCBI_Taxid=75985;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=PR278;		
RX	MEDLINE=21101823; PubMed=11157953;		
RA	Davies R.L., Whittam T.S., Selander R.K.;		
RA	"Sequence Diversity and Molecular Evolution of the leukotoxin (lktA)		
RT	Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)		
RT	haemolytica";		
RL	J. Bacteriol, 183:1394-1404(2001).		
DR	EMBL; AF314514; AACG40298.1;		
DR	InterPro; IPR001753; Enoyl-CoA_hydrtse.		
DR	InterPro; IPR001343; HemIysN_Ca_bind.		
DR	InterPro; IPR003355; RTX_N.		
DR	Pfam; PF00353; hemolysinCdbind; 1.		
DR	Pfam; PF02382; RTX_1		
DR	PRINTS; PR00313; CAENDNGRPT.		
DR	PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.		
SEQ	SEQUENCE 953 AA: 102147 MW: 11600FDA7849AICA CRC64;		

[illegible]

QY	302	KFNHNAHLDPEAKQFRKFRGVDGHLAEYRGQVGTIDASLTITTTALGAVSAGVSAANV	361
Db	320	KFNHAKSLSESAEFAEFKRLGYDGMLLAEYRGVGTIDASVTALNTALAAIAGVSAAG	379
QY	362	SAVAGPITALVAGVTGLISGLLEASQAMFESVANRLQGLILEWKGONGGONFEDKGYDS	421
Db	380	SVASPIALLVSGTITVSTILOYSKQAMFEHVANKIHNKIIVEMEKNNHKNKFNENGYDA	439
QY	422	RYAAVLANNILKFLSELKLEAEFVIAITQQRMDNIGELAGITTKGERIKSGKAVADAF	481
Db	440	RYLANLOQNMKFLNLNKLELOAEFVIAITQOQMNINIGDLAGISRLQEKVLSKAYADAF	499
QY	482	EDGKRVKVEGSMITTDARTGIIIDINSNGKQALHFTSPLITGTGTESEHFLTNKYSYN	541
Db	500	EEGKIKTKADKLVQDDSAANGIIVDSNSGKQAHITFLPTLPETGERHERVOTGKEIYIT	559
QY	542	KLKFERVYNQVOTGTEGASSKIDFESKVIQVR-----AETEGTDEIGLIYNAGANDIF	594
Db	560	KLINIRVDSKMITTQGAASSTFDLINVQRIEILDNMGNTVKTETKIILAKLGGDDNVF	619
QY	595	VGGQKMNIDGDDGHDVRYFYSKDGEGFNITVDGTSATAGSYTVNRKARGDYIHEVYKRQ	654
Db	620	VSGTTEIEDGEGYDRAVYSR-GNYGALTIDATETEGSGSYTVNRFEYTGALHEVYSTH	678
QY	655	ETKVKRTEITQYRVELRKVGYGVQSDNKLKSEEVYVGSOFNVFVFGSKFNDFHSHGEG	714
Db	679	TALVNSRREKEIEYR-HSNQNHAGIYTKDLKABEITIGTSHNDIFFGSKFNDAFNGDGG	737
QY	715	DLLDLGGCGADRLFFGKGNDRLLSGDEGDDLLDGGSGDDVNLGGAANDVYITFRKGDNDTL	774
Db	738	VDTIDGNGNDRLFRGCKGDDLLDGGNGDDFIDGGKGNDDLHGGGDDIFVHRKKGNDII	797
QY	775	YDGTGNDKLAFRDNANISDIMIERKEGIIYVRNDHSGSINIPRY-----ITSNLQNTQSN	833
Db	798	TDSDDNDKLTFSFSDSNLMDLTPEFKYHNLYI-TNSKKEKVTIQQDFREADFAKEVPNKAT	856
QY	831	KRDHKITEQIDGDSYITSDIDKTLQDKKGTGYITSOELKRLDENKSKQSLASDIASS	890
Db	857	K-DEKIEETELIGONGRITRSKQVDDLI--AKNGKGTIDQELSKYVDNDELKHS-KVNTNS	912
QY	891	LNKLIVSGMALFGTANSVSSNALQPIPTQPTGCI	922
Db	913	LDKLSSVSAFTSSNDSRNVLVAPTSMLDQSL	944
RESULT 14			
Q9EY34 PRELIMINARY; PRT; 953 AA.			
AC	Q9EY34:		
DT	01-MAR-2001 (Tremblrel. 16, Created)		
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)		
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)		
DE	LEUKOTOXIN.		
GN	LKTA.		
OS	Pasteurella haemolytica.		
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;		
OC	Mannheimia.		
OX	NCBI_TaxID=75985;		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=PH56;		
RX	MEDLINE=21101823; PubMed=11157953;		
RA	Davies R.L., Whitlam T.S., Selander R.K.;		
RT	"Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)		
RT	Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)		
RT	haemolytica.";		
RL	J. Bacteriol. 183:1394-1404(2001).		
DR	EMBL; AF314505: AAG40289.1. -		
DR	InterPro; IPR001753; Enoyl_COA_hydrtase.		
DR	InterPro; IPR001343; Hemolysin_Ca_bind.		
DR	InterPro; IPR003355; RTX_N.		
DR	Pfam; PF00353; hemolysinCbind; 1.		


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Db 500 EEGHKLADKLVLQDSANGIIVDSNGKAKTOHILFRPLLPCTEKKRERVOTGKYXYIT 559
Qy 542 KLRGVRVNMQVOTDGEASSKIDFSKIORV-----AETEGTDEIGLIYAKAGNDIIF 594
    || :||:||||| || :||:
Db 560 KLINRVDMSKIDTGEASTDILTNVORIGIELDNAGNVTKTETKIIAKLGEGDNIIF 619
    || :||:||||| || :||:
Qy 595 VGGKMNIDGGDGHDRVFFYSKDGSGFNITVDGTSATENGASYTNRKVARGDIYHEVYKRO 654
    || :||:||||| || :||:
Db 620 VSGGTIELDGESEYDRVHYSR-GNYGALIIDATKETEGSYTVNRFEVETGKALHEVSTH 678
    || :||:||||| || :||:
Qy 655 ETAVGKRTETIQYRDYELRAVGYGQSTDNLSKVEEYIGSQPNDFKSGKFNDFHSGEG 714
    || :||:||||| || :||:
Db 679 TALVGSREKTEYRHSNNROHA-GYTKDTLTSIEELIGTSHNDIFKGSQPNDAFNGDG 737
    || :||:||||| || :||:
Qy 715 DDLDDGAGDDRLFGGKGNDRLSGDEDDLDDGSGDDVNLNGAGANDVYIFRKGDNDTL 774
    || :||:||||| || :||:
Db 738 VDTIDGNGNDRLFGGKGDIIIDGGDDPFDGKGNLDLHGKRGDDIFVHRGSDGNDISI 797
    || :||:||||| || :||:
Qy 775 YDGTGNDRKLPADANISDIMIERTEKEGIIVRKNDHSGSINIPRWY---ITSNLQNYQSN 830
    || :||:||||| || :||:
Db 798 TEAGGHDRLSFDLSNKLDTFEKVNHLYI-TNTKQEKVTIONMFRREEFKATVKNYVAT 856
    || :||:||||| || :||:
Qy 831 KTDHRIEOLIGKDGSYTSDQIDKILQDKD-----GTVITSQELKKLADENKSOKL 882
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Db 857 R-DEKIEELIGONGERITSKQVDELIAGKDNKIDKNDLANVANSYELLK----- 905
    || :||:||||| || :||:
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    || :||:||||| || :||:
Db 906 NSRNVNLSLKLISVSSFTSSND-SRNVL 934
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Search completed: September 11, 2002, 09:01:25
 Job time: 283 sec

Db 173 QSLTQAG-SSLTGAKKILLYIPONTQYDTGQNGIQLDLYKAAEELGIEVQREERNINAT 231
QY 66 AKRSVTVNOFLSLTQTGIALSATKLEKFLQKHSITNKLAKGLDSEVNDIKLKASNVLS 125
Db 232 AQTSLGTIQTALITLTERGIYLSAPQIDKLQK---TKAGALGSASESIYONANKAKTVLS 288
QY 126 TLSSFLGTALAGIELDSLIRKGAAPADALAKASIDLINETIGNLSOSTQTIEAFSSOLAK 185
Db 289 GIOSIIGSVIAGMDLDEAL-ONNSNOHALAKAGLELINSLENIANSVKTLDEFGDISQ 347
QY 186 LGSTISQAKGFSNIGNKLONL-NFSKTNLGLTITGLSGISAGFALADKNASTGKVVAA 244
Db 348 FGSKLONIKGLTIGDKLKNIGLDRAGLGLDVIYSGLLSATAIYALADKNASTAKVGA 407
QY 245 GFELSNQVGNITKAVSSYIIAQVAGLSTGFPVALLASTVSLASTPLAFAGIDKFN 467
Db 408 GFELSNQVGNITKAVSSYIIAQVAGLSTGFPVALLASTVSLASTPLAFAGIDKFN 467
QY 305 HANALDEFAKQFRKFGDGHLLAEYORGVTIEASTITSTALGAVSAGVSAAVSAY 364
Db 468 HAKSLESTAEERKFLGYDGNLLAEYORGVTIDASVTAINTALAAIAGVSAAGVSAVI 527
QY 365 GAPILALVAGVTGLSIGILEASKQAMFESVANRLOGKILEMEKONGQNTYFDKYSRYA 424
Db 528 ASPILALVSGIYVSTILOYSKQAMFEHVANKIHNKIVEMEKNNHGKNYFENGADARYL 587
QY 425 AYLANNLKFLSELNKELEAEVIAITTOORNDNINIGELAGITKGERIKSKAYADAFEDG 484
Db 588 ANLQDNMKFELNLNKELEAEVIAITTOOQWNNIGLAGISRLGEKVLGSKAYADAFEEG 647
QY 485 KKVAGSNTITDAKTGIIDISNSNGKTKQALHFTSPILTACTESRETRLNKSYINKLK 544
Db 648 KHTRADKLVOJDSANGIIVDSNSKAKTOHILFTPLTPTREHREYQVQIKYITIKLN 707
QY 545 FGKVKMVOYTDGEASSKIDFSKYQVR-----AETEGTDELGLYNAKAGNDIYVQ 597
Db 708 INRVDSMKITDGAASSTFDLTNNVQRIEELDNAGNVTKETKRIKIALGEGDNNVFGS 767
QY 588 GKMNIDGSDGHDVRFYKSDGSGFNTVDTGTSATEAGSYTVARKVARGIYHEVYKROETK 657
Db 768 GTTELIDGEGYDRIYHVR-GNKGALTIDATKETEGSGTYVNRVEYTGALHEVSTHIAL 826
QY 658 VGRFTETIYQDYELRKRYGYQSTDNLSKVEEYIGSOFNDFVFKSGKPNDFHSGEGDL 717
Db 827 VGNREKTEYR-HSNNOHAGIYGTDTLKAVEIIGTSHNDFKSGKPNDAFNGSDGYDT 885
QY 718 LDGAGDRLFGKGNDRILSGDEGDLDDGSGDVIYNGAGNDVIYIRKGGNDTLYDG 777
Db 886 IDGNGDNRLFGKGGDDLLDGGNGDDFDIDGKGNLHGGKDDLFVHRKGGNDIITDS 945
QY 778 TGNDKLAFADANISIMIERTEKGIITVRNDSGSIINIPRWY---ITSNLQNYOSNKT 833
Db 946 DGNDLSTSDSLUKDLTPEKYNHNLVI-TNSKKEVYTIOMNFRADPAKEYVNYKATK-D 1003
QY 834 HKIEOLIGKDSYITSDDIKLIDKDCGTVITSQELKKLADENKSQKLSASDIASLNLK 893
Db 1004 EKIEELIIGNGRITSKYQVDLI--AKNGKITODELSKRVYDNYELLKHS-KNYVNSIDK 1060
QY 894 LVGSNALFTANSVSSNALQPTQPTQGI 922
Db 1061 LISSVAFSTSSNDSRVNLVAPTSMLDQSL 1089

RESULT 2
US-08-170-126-2
; Sequence 2, Application US/08170126
; Patent No. 5594107
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW
; APPLICANT: CAMPOS, MANUEL
; APPLICANT: HUGHES, HDM P.A.
; TITLE OF INVENTION: CYTOKINE-CYTOTOXIN GENE FUSIONS AND USES
; TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,126
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/777,715
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/571,301
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0013.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-170-126-2

Query Match 50.2%; Score 2334; DB 1; Length 1098;
Best Local Similarity 50.1%; Pred. No. 8, 8e-175;
Matches 465; Conservative 175; Mismatches 263; Indels 26; Gaps 13;

QY 8 KSNQAGLNSKSGSKLMLYLAIPKD--YDPQKGTLDNDFKADDELGIARIAEPNHTEY 65
Db 173 QSLTQAG-SSLTGAKKILLYIPONTQYDTGQNGIQLDLYKAAEELGIEVQREERNINAT 231
QY 66 AKRSVTVNOFLSLTQTGIALSATKLEKFLQKHSITNKLAKGLDSEVNDIKLKASNVLS 125
Db 232 AQTSLGTIQTALITLTERGIYLSAPQIDKLQK---TKAGALGSASESIYONANKAKTVLS 288
QY 126 TLSSFLGTALAGIELDSLIRKGAAPADALAKASIDLINETIGNLSOSTQTIEAFSSOLAK 185
Db 289 GIOSIIGSVIAGMDLDEAL-ONNSNOHALAKAGLELINSLENIANSVKTLDEFGDISQ 347
QY 186 LGSTISQAKGFSNIGNKLONL-NFSKTNLGLTITGLSGISAGFALADKNASTGKVVAA 244
Db 348 FGSKLONIKGLTIGDKLKNIGLDRAGLGLDVIYSGLLSATAIYALADKNASTAKVGA 407
QY 245 GFELSNQVGNITKAVSSYIIAQVAGLSTGFPVALLASTVSLASTPLAFAGIDKFN 467
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QY 305 HANALDEFAKQFRKFGDGHLLAEYORGVTIEASTITSTALGAVSAGVSAAVSAY 364
Db 468 HAKSLESTAEERKFLGYDGNLLAEYORGVTIDASVTAINTALAAIAGVSAAGVSAVI 527
QY 365 GAPILALVAGVTGLSIGILEASKQAMFESVANRLOGKILEMEKONGQNTYFDKYSRYA 424
Db 528 ASPILALVSGIYVSTILOYSKQAMFEHVANKIHNKIVEMEKNNHGKNYFENGADARYL 587
QY 425 AYLANNLKFLSELNKELEAEVIAITTOORNDNINIGELAGITKGERIKSKAYADAFEDG 484
Db 588 ANLQDNMKFELNLNKELEAEVIAITTOOQWNNIGLAGISRLGEKVLGSKAYADAFEEG 647


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:      REGISTRATION NUMBER: 33,208
:      REFERENCE/DOCKET NUMBER: 9000-0026
:      TELECOMMUNICATION INFORMATION:
:      TELEPHONE: (415) 617-8999
:      TELEFAX: (415) 327-3231
:      INFORMATION FOR SEQ ID NO: 2:
:      SEQUENCE CHARACTERISTICS:
:      LENGTH: 926 amino acids
:      TYPE: AMINO ACID
:      TOPOLOGY: linear
:      MOLECULE TYPE: protein
:      US-07-908-253-2

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183 IKGGTGLDGLKNGIDKAGLGLDVISGLSGATLALVLADKNAATKAVGAGFELANQ 242
252 VIGNVTKAISSYLAORVAAGLSTTGAVAAALITSSIMLAISPLAFMAADKFNHANA 311
243 VVGNTTAVSSYLLAORVAAGLSTGVAALIASTVLAISPLAFAGIADKFNHAKSLES 302
312 FAKOFRKFGYDGHLLAEYQGVGTIEASLTITSTALGAVSAGVSAAGVAVGAPITAL 371
303 YAEFRKLLGYDGNLLAEYQGVGTIDASVTAINTALAAIAGVSAAGVAVGAPITAL 362
372 VAGVTGLISGLTEASKOAMFESVANRLOGKILEWEKONGQONFVPGKYSRYAAYLAN 431
363 VSGITGVISTILQYSKOAMFHVANKIHNNKVEWEKNNHGNKNYENGDAVYLANLQDM 422
432 KFLSELNKELEAERVIAITQOOWMNNIGLAGISRLGEKVLGSKAYVDAFEKGHIKAD 482
423 KFLNLNKELEAERVIAITQOOWMNNIGLAGISRLGEKVLGSKAYVDAFEKGHIKAD 482
492 NITDAKTGIIDISNSNCKTQALHFTSPLLTACTESERLTNGKYSYINKLFGRYKNW 551
483 LVQDLSANGIIDVNSNGAKTQHLIFRPLTPGTEHREKQVOTGKEYITKLNINRDSW 542
552 QVTGGEASSKIDFSKVIOQV-----AETGTEDEIGLIVAKAGNDIFVGGKMNIDG 604
543 KITGGAASSTFDLTNVQVRIGIELDNAGNVTKTKETKILIAKLGEGDDNVFVSGTTEIDG 602
605 GDGHDVRFYSKDGFGNTVDGTSATEAGSTTVNKRKARGLIYHEVYKROETKYGKRET 664
603 GEGYDRVHYSR-GNYGALTIDATKETEQGSYTVNKFVETGALHEVYSTHVALGNREK 661
665 IOYRDELRYKGYGYOSTDNLKSEVEYIGSOFNDVFKSGKNDIFHSGEGDLDLGAGD 724
662 IEFR-HSNNOHAGIYTDLTAKAVEIIGTSHNDIFKSGKNDIANGDGDVDTIDGNGN 720
725 DRLFGKGNDRISGDEGDDLDGSGDDVNLGAGANDYIIRKQDGNNTLDGKNDKLA 784
721 DRLFGKGGDDLDGNGGDDFDLGKGNDDLHGKGGDIFVHRKGGNDIITDSGNDLS 780
785 FADANISDIEMERTKEGIIIVKRNDSGSIINPRW----ITSNLQNSYNTDHIKLEOLI 840
781 FDSNMDKIDLPFKYKHNLYI-INSKKEVYTIQNWFRADFAKEVYNYATK-DEKIEELI 838
841 GKDSYITSDOIKLIDKQDGTVITTSOLKKLADENKSOKLISASDIASLKLKLVGSMAL 900
839 GQNGRITSKYVDLI--AKNGKITDDELASKVDNYELLKHS-KNVTNSIDKLISVSA 895
901 EGTANSVSSNALQITPOTPOGI 922
896 FTSSNDSRNVLVAPTSMDOSL 917

RESULT 7
US-08-387-156-6
; Sequence 6, Application US/08387156
; Patent No. 5723129
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HOW P.A.
; TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-387-156-6
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Query Match 50.1%; Score 2326.5; DB 1; Length 926;
Best Local Similarity 50.0%; Pred. No. 2,6e-174;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;

15 LNSTKSLKLNLYAIPD--YDPQKGTINDPFIKADELGIALAEENPTETAKKSVDP 72
7 LSPFKTGAKKILIVLPONYQYDTEQNGLDLVKAAEELIEVORENNIATATQISLGT 66
73 VNCGLSTGNGIAISATKLEFKLOKHSNTKLANGLDSVENIDRKLGASVNLSTLSSFLG 132
67 IQTAIGLTERGIYVSAQIDKLLQ---TKAGALGSAESIYONANKAKTVLSIGISILG 123
133 TALAGIELDSTLRKGDAPDALAKASIDLINEITGNLSOSTQTIEARSSQALKGTSIQ 192
124 SYLAGMDLDEAL-ONNSNOHALAKAGLENTSLIENIANSVKTLDEGEQISQGSYLNQ 182
193 AKGFSNIGNKRLQNL-NFSKTNLGLIEITGLSGISAGFALADKNAKSGKRVAGFELSNQ 251
183 IKGGTGLDGLKNGIDKAGLGLDVISGLSGATLALVLADKNAATKAVGAGFELANQ 242
252 VIGNVTKAISSYLAORVAAGLSTTGAVAAALITSSIMLAISPLAFMAADKFNHANA 311
243 VVGNTTAVSSYLLAORVAAGLSTGVAALIASTVLAISPLAFAGIADKFNHAKSLES 302
312 FAKOFRKFGYDGHLLAEYQGVGTIEASLTITSTALGAVSAGVSAAGVAVGAPITAL 371
303 YAEFRKLLGYDGNLLAEYQGVGTIDASVTAINTALAAIAGVSAAGVAVGAPITAL 362
372 VAGVTGLISGLTEASKOAMFESVANRLOGKILEWEKONGQONFVPGKYSRYAAYLAN 431
363 VSGITGVISTILQYSKOAMFHVANKIHNNKVEWEKNNHGNKNYENGDAVYLANLQDM 422
432 KFLSELNKELEAERVIAITQOOWMNNIGLAGISRLGEKVLGSKAYVDAFEKGHIKAD 482
423 KFLNLNKELEAERVIAITQOOWMNNIGLAGISRLGEKVLGSKAYVDAFEKGHIKAD 482
492 NITDAKTGIIDISNSNCKTQALHFTSPLLTACTESERLTNGKYSYINKLFGRYKNW 551
483 LVQDLSANGIIDVNSNGAKTQHLIFRPLTPGTEHREKQVOTGKEYITKLNINRDSW 542
552 QVTGGEASSKIDFSKVIOQV-----AETGTEDEIGLIVAKAGNDIFVGGKMNIDG 604
543 KITGGAASSTFDLTNVQVRIGIELDNAGNVTKTKETKILIAKLGEGDDNVFVSGTTEIDG 602
605 GDGHDVRFYSKDGFGNTVDGTSATEAGSTTVNKRKARGLIYHEVYKROETKYGKRET 664
```



```

CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,748
FILING DATE: 19-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3231
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-878-748-6

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Query Match          50.1%; Score 2326.5; DB 2; Length 926;
Best Local Similarity 50.0%; Pred. No. 2.6e-174;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;

QY 15 LNSTSGKLNLYLAIKPD--YDPQGGTINDRIKADDELGTARLKEEPNHTTAKSVDT 72
DB 7 LSEPTGAKILLYIPQNYDTEQNGIQLDYKAAEEGLIVOREERNNTATQTSIGT 66
QY 73 VQOFLSLQOTGIAISATKLEFKLKHSTNKLAKGLDSVENIDRKLGKASNYLSTLSFGL 132
DB 67 IOTAIGLIRGIVLAPQIDKLQK--TKAQALGSAESIYQNNKKTIVLSGIGSLIG 123
QY 133 TALAGTIDSLIKGDADALAKASIDLINEITGNLSOSTIOTIAFSSQLAKGSTISQ 192
DB 124 SYLAGMDLDEAL-QNNNSOHALAKAGLELTNSLINIANSVKTLDLFEFGQISQFGSKION 182
QY 193 AGFSGNIGKLNLT-NFSNTNIGLEITGLSGISGAFRLADKNASTGKVAAGSELSQ 251
DB 183 IIGLGLTGKLNIGGLDAGLGLDYLISGLSGATRALVALADKNASTAKKVAAGFELANQ 242
QY 252 VIGNVTAKSSYVLQRYVAGSLTGGAVALLTSSIMLAISPAPMNAADKENHANALDE 311
DB 243 VVGNTITKAVSYTLQRYVAGSLTGGAVALLTSSIMLAISPAPMNAADKENHANALDE 302
QY 312 FAKQFKFGYDGDHLAEYQRYGVTIEASLITSTRALGAVSAGVSAANAGVAPIAL 371
DB 303 YAEERFKLGYDDNLAELAEYQRYGVTIEASLITSTRALGAVSAGVSAANAGVAPIAL 362
QY 372 VAGVTIGSLILEASKQAFESYANRLQKTIEMERKONGQVYFDPKGYDSRAAYLAN 431
DB 363 VSGITIVISTIIQYKQAFENYANKIHKKIYEMENNNKGYFENGYIARLANIQDM 422
QY 432 KFLSELNKELEERVAITQORNDNIGELAGITTKLGERIKSGKAYADA FEDGKVEAGS 491
DB 423 KFLNINKELEERVAITQOQNDNIGLGLAGISRLGEKAVYLSGKAVYDAFEKGKHKADK 482

```

```

QY 492 NITLDAKTGILIDISNSGKKTQALHFTSPLLTAGTESRERLTNGKSYINKLKFGYKMW 551
DB 483 LVQIDANGILIDVNSGKAKTOHILFRPLTPTGTEHREVRVQTKYEYITKLKININ 542
QY 552 QYTDGEASSKLDPSKYIQR-----AETEGIDELGLYNAAGNDLFFVGKKNING 604
DB 543 KITDGAASSTFDLTNNVQRIQIELDNAGVNTKTKETKIILAKLGEDDNVFGSTTEIG 602
QY 605 GDGHDYRVEYKDGFGFNITVDGTSATEAGSYTVNRKVARGDYIEYVKRQETKVGRTET 664
DB 603 GEGYDRHYER-GNYGALITIDATKETEGSYTVNRFVETGKALHEVTSFTHALVGNREEK 661
QY 665 IQRYDELRKRVGYGYSTDNKSYVEEYTGSEFNDYKRGKSFNDIPIHSGEEDLLDGGAD 724
DB 662 IEYR-HSNNOHHAGYTKDILKAVEELITGSHDIFGSKFNDAFNGDGVDPIDNDGN 720
QY 725 DRLEGGKGNRLSGDEGDDLLDGGSGDDVANGANDVYIFRRKGDNDLTLDGTGNDKLA 784
DB 721 DRLEGGKGDLLDGGNDDDTLDGKGNDLHGKGGDIFVHRKGDNDITLSDGNDKLS 780
QY 785 FADANISDIMERTREGIIVKRDHSGSINIPRWY---ITSMLQNYQSKTKDHTIEOLI 840
DB 781 FSDSNLMDLFEKVKHNLVI-TNSKREKVTIOWMFREADFAKEVPYKATK-DEKIEEII 838
QY 841 GKDSYITSDQIDKILDDKDGIVYTSQELKTLADENKSKGLASDASSLNKLTVGSMAL 900
DB 839 GQNERITTSQVDDL--AKNGKITODELSKVVDNYELKHS-KVNTNSLDKLSSVA 895
QY 901 FGTAHSVSNALQPIPTOPTGI 922
DB 896 FTSSNDSRNVLVAPTSLMDQL 917

```

```

RESULT 10
US-08-535-837-2
Sequence 2, Application US/08535837
Patent No. 5985289
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,837
FILING DATE: 27-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0026.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-535-837-2

```


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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:55:36 ; Search time 75.59 Seconds
(without alignments)
1362.156 Million cell updates/sec

Title: US-09-884-696-2

Perfect score: 4646
Sequence: 1 MSNINVTKSNTQAGLNSTKS.....SSNALQPTPTQGLAPSV 927

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq.032802:*

1:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
2:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
3:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
4:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
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9:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*
10:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*
11:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
12:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*
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16:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*
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18:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
19:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
20:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
21:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22:	/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4642	99.9	927	22	AAB62110
2	2334	50.2	1098	18	AAW13866
3	2334	50.2	1098	21	AAW21073
4	2332	50.2	1098	13	AAW21073
5	2329	50.1	953	14	AAW3865
6	2327	50.1	1098	15	AAW52747
7	2326.5	50.1	924	14	AAW42385
8	2326.5	50.1	924	14	AAW42380
9	2326.5	50.1	924	14	AAW42378
10	2326.5	50.1	926	12	AAW14482
11	2326.5	50.1	926	14	AAW34545

12	2326.5	50.1	926	15	AAW50291	Recombinant leukot
13	2326.5	50.1	926	19	AAW79568	Leukotoxin 352 pol
14	2326.5	50.1	977	17	AAW03942	LKT-GnRH protein f
15	2326.5	50.1	977	19	AAW79569	LKT-GnRH chimeric
16	2326.5	50.1	1069	15	AAW52748	Bovine IFNgamma/LK
17	2326.5	50.1	1069	18	AAW13867	Chimeric protein #
18	2326.5	50.1	1069	21	AAW21074	Bovine gamma-IFN/P
19	2325	50.0	953	11	AAW07167	105KD PTX protein
20	2325	50.0	953	15	AAW60072	PLX protein of Pa
21	2325	50.0	953	22	AAW04638	Pasteurella haemol
22	2323.5	50.0	943	14	AAW34546	Somatostatin-leuko
23	2318.5	49.9	936	14	AAW34547	GnRH-leukotoxin ge
24	2317.5	49.9	924	12	AAW10889	Leukotoxin 352 enc
25	2317.5	49.9	924	12	AAW03945	P. haemolytica tru
26	2313	49.8	953	17	AAW15159	Leukotoxin from P.
27	2312.5	49.8	951	14	AAW34548	Leukotoxin VP4-leuk
28	2301.5	49.5	934	17	AAW07637	P. suis leukotoxin
29	2240.5	48.2	956	12	AAW12661	APPA haemolysin an
30	2240.5	48.2	956	18	AAW22156	Apptic protein. A
31	2240.5	48.2	956	21	AAW51410	A. pleuropneumonia
32	1928	41.5	1049	18	AAW22159	ApixiIB protein.
33	1928	41.5	1049	21	AAW51412	A. pleuropneumonia
34	1928	41.5	1244	15	AAW54781	Leukotoxin Appiia
35	1767.5	38.0	1022	18	AAW22152	Apixia protein. Ac
36	1767.5	38.0	1022	21	AAW51406	A. pleuropneumonia
37	1731	37.3	1023	16	AAW76891	Lhaa (low homology
38	1464.5	31.5	608	22	AAW04636	Pasteurella haemol
39	1380.5	29.7	758	17	AAW86998	Enterohaemorrhagic
40	1159.5	25.0	450	22	AAW04637	Pasteurella haemol
41	904.5	19.5	544	19	AAW79570	LKT-GnRH chimeric
42	901	19.4	695	19	AAW79573	LKT-GnRH chimeric
43	901	19.4	695	21	AAW58361	Leukotoxin/gonadot
44	901	19.4	695	21	AAW58333	Gonadotropin relea
45	897.5	19.3	490	20	AAW39529	Leukotoxin carrier

ALIGNMENTS

RESULT	1
AAW62110	standard: Protein; 927 AA.
ID	AAW62110:
AC	AAW62110:
DT	29-MAY-2001 (first entry)
DE	M. bovis Dalton 2d RTX toxin A subunit.
XX	
KW	Moraxella: antigen; immune response; infection; RTX toxin; vaccine;
KW	antibacterial; A subunit.
XX	
OS	Moraxella bovis.
PN	MO200116172-A1.
XX	
PD	08-MAR-2001.
XX	
PF	31-AUG-2000; 2000MO-AU01048.
XX	
PR	31-AUG-1999; 99AU-0002571.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
PA	(UYME) UNIV MELBOURNE.
PI	Farn J, Strugnell R, Tennent J;
XX	
DR	WPI, 2001-235092/24.
XX	
PT	N-PSDB; AAF57290.
XX	
PT	Novel Moraxella bovis antigen useful in compositions for raising immune
XX	response in an animal, has protease, lipase or hemolysin activity

PS Claim 26; Fig 5; 60pp; English.

XX The invention relates to new Moraxella bovis antigens and nucleic acid
 CC sequences encoding these antigenic polypeptides. The antigenic
 CC polypeptides and polynucleotides are useful for raising an immune
 CC response in an animal directed against Moraxella, preferably against
 CC M. bovis or M. catarrhalis, and for treating Moraxella infections. The
 CC present sequence represents the amino acid sequence of the A subunit of
 CC the RTX toxin from M. bovis Dalton 2d.

XX
 XX Sequence 927 AA;

Query Match 99.9%; Score 4642; DB 22; Length 927;
 Best Local Similarity 99.9%; Pred. No. 2.4e-294;
 Matches 926; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSNINVIKSNIOAGLNTSKSLKMLYLAIKPYDPOKGTLDNFIKADDELGIARLAEEP 60
 DB 1 msninviaknlgaglnstkslknlylaipkydpqkgylndfikaadelgiarlaeep 60
 OY 61 NHETAKSVDTVNOGFLSTOTGIAISNTKLEKFLQKHSSTKLAKGDSVENIDRKIGKA 120
 DB 61 nhetaksvdtvnoqflstotgiaisntklekflqkhsstklakgdsvenidrkigka 120
 OY 121 SNVLTSSFLGTALAGIELDLSLIRKGDAPADALAKASIDLINELIISNLSOSTOTTEAFS 180
 DB 121 snvltssflgtalagieldlsllirkgdapadalakasidlinelignlsostqtieafs 180
 OY 181 SOLAKLGSTISQAKGFNSIGNKILQNLNFSKTNLGEITLGLSGISAGFALADKNASTGK 240
 DB 181 solaklgstisqakgfnsignkqlnlnfsktnlgeitlglsgisagfaladknaastgk 240
 OY 241 KVAAGFELSNQVIGVNTKAISSYVAQVAAGLSTGVAALITSSIMLAISPAPFMAA 300
 DB 241 kvaagfelnsqvigvntkaiissyvaqvaaglstgvaalittssimlaspapfmaa 300
 OY 241 kvaagfelnsqvigvntkaiissyvaqvaaglstgvaalittssimlaspapfmaa 300
 OY 301 DKFNHANAIDFEAKOFRKFGYDGDHLAEYORGVGTLIASLTITSTALGAVSAGVSAAV 360
 DB 301 dkfnhanaidfeakofrkfgydgdhlaeyorgvgtliasltitstalgavsagvsaav 360
 OY 361 GSANGAPIALLVAGYTGILSIGILEASKAMFESVANRQKRTILEMEKNGCONVFDKGYD 420
 DB 361 gsangapiallvagytgilsigileaskamfesvanrqrtilemekngconvfdkgyd 420
 OY 361 gsaavtptallvagytgilsigileaskamfesvanrqrtilemekngconvfdkgyd 420
 OY 421 SYAAAYLANNNKFLSELNKELEAEKVIAITQORMDNNGELAGITRKLERIKSGKAVADA 480
 DB 421 syaaaylannnkflselnkeleaeerviaitqorwmdnnigelagitkgeriksgkayada 480
 OY 481 FEDGKRKVEAGSNITLDAKTGIIIDISNSNGKTOALHFTSPLLTACTESREKLTNCKYGI 540
 DB 481 fedgkrkveagsnitldaktgiiidisnsgktoalhftsplltactesrerltngkygi 540
 OY 541 NMLTKGRVKNQVDTGGEASSKLDPSKVITQORVAETGETBIEGLIVAKAGNDIIFGQGGK 600
 DB 541 nmltkgrvknqvdtggeasskl dpskvitqorvaetgetbieglivakagndiifvggkm 600
 OY 601 NIDGGDHDVRVFSKDGSGNTVDGTSATEAGSYTVNKKVARGDIYHEVVKRQETVYK 660
 DB 601 nidggdhdvrfskdgsngntvdgtsateagsytlvnkkvargdiylhevkrqetvkgk 660
 OY 661 RRETIOYRDYELRKVGYGQSTDNLKSVEVEIGSQPNVFKSKRNDRTHSSEGGDLDG 720
 DB 661 rretioyrdyelrkvgygqstdnlksveveigsqpndvfkskrndrthsseggdldg 720
 OY 721 GAGDDRLFEGKGNDRSGSEGDDLDGGSDDVVLNKGAGNDVYIFPKGNGNTILVDTGN 780
 DB 721 gagddrlfegkgndrsgegddldggddvvlngkagndvyifpkngntilvdgtgn 780
 OY 781 DKLAFADANISDIIMERTEGIIIVKRNHSGSINIPRWYITSNLQYNSKNTDKHIEQLI 840
 DB 781 dklafadanisdiiimertegiiivkrnhsgsiniprwyitsnlqynskntdkhieqli 840

OY 841 GKDSYITSDQIDKILDDKDKDGTVTTSQELAKRLADENKSQKLSASDIASLNKLKVSMA 900
 DB 841 gkdsgyitsdqidkildddkdkdgtvttsqelakrladenksqklsasdiasslnklkvsma 900
 OY 901 EGTANSVSSNALQPTPQPGIILAPSV 927
 DB 901 egtansvssnalqptpcpgiilapsv 927

RESULT 2

AAW13866 standard; Protein; 1098 AA.

AAW13866;

12-MAY-1997 (first entry)

Chimeric protein #1.

RTX cytotoxin; cytokine; immunogen; chimeric protein; cytokine; vaccine;
 Interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; pneumonia;
 Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;
 fibrinous pneumonia; cattle; therapy.

Synthetic.

US5594107-A.

14-JAN-1997.

22-AUG-1990; 90US-0571301.

20-DEC-1993; 93US-0170126.

22-AUG-1990; 90US-0571301.

16-OCT-1991; 91US-0777715.

(CIBA) CIBA GIEGY CANADA LTD.

(UTSA-) UNIV SASKATCHEWAN.

Campos M, Hughes HPA, Potter A;

WPI; 1997-099529/09.

N-PSDB; AAT60032.

Immunogenic chimeric proteins comprising cytokine linked to RTX

toxin - useful in vaccines, esp. against shipping fever in cattle

Claim 10; Column 25-32; 56pp; English.

AAW13866 and AAW13867 represent immunogenic chimeric proteins of the
 invention. This sequence represents a chimeric protein containing the
 bovine interleukin-2 (IL-2) sequence and a leukotoxin sequence. The
 chimeric proteins of the invention comprise a cytokine, selected from
 IL-2 and gamma interferon (gamma IFN), linked to at least one RTX toxin
 epitope (preferably the sequence shown in AAW13865). The RTX toxin used
 to provide the epitope sequence is preferably a leukotoxin, especially
 the full-length Pasteurella haemolytica leukotoxin. Alternatively, the
 leukotoxin is a truncated leukotoxin lacking leukotoxic activity,
 especially LKT352. The chimeric proteins can be used for the production
 of vaccines against respiratory diseases such as pneumonia, particularly
 fibrinous pneumonia caused by P. haemolytica, including shipping fever in
 cattle.

Sequence 1098 AA;

Query Match

Best Local Similarity 50.2%; Score 2334; DB 18; Length 1098;

Matches 465; Conservative 175; Mismatches 263; Indels 26; Gaps 13;

OY 8 KSNIOAGLNSTKSGIKNLTYLAIPKD--YDPOKGTLDNFIKADDELGIARLAEEPNHET 65
 DB 173 gsltgag-salktgaklillyipnyqy/dteqnglqdlvkaaeelgievgreenmlat 231

```

OY 66 AKKSVDTVNOFLSLTQGTGIAISATKLEKFLQKHSTNKLAKGLDVENIDRKLKASNVLS 125
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 232 aqstlgtltaigtalgttergylvlsapqdkllqk---tkagqalgsaesiynanakkatvls 288
OY 126 TLSSFLGTALAGIELDSLIRKGDAPDALAKASIDILINELTGNLSOSTOTIEAFSSQLAK 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 289 gtslilgsvlaqmdleal-qmnsqhalaqkajeltlnsleniansvktldeffgeqisq 347
OY 186 LGSTISQAGFSNIGKNLONL-NFSKTNLGLTITGLSGISGFPALADKNASTGKRVAA 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 348 fgsqkqnlgytlgdklknlgldkaglgldvlsqllsgataalvldaknastakvga 407
OY 245 GFELSNQVIGNVTKAISSVYLAQVAAGLSTTGAVAAALITSSIMLAISPLAFNAAADKFN 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 408 gfeianqvgvnltkavssyllaqgrvaaglsstgvpvaallastcslsplsafagjadtfn 467
OY 305 HANAIDFAKOPRRFGYDGDHLLAEYQRGVGTTEASLTITSTALGAVSAGVSAAVGSAV 364
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 468 hakslesyaerfkklygdgdnllaeygrgtgltidasvtaintaalaagvsaaagsvyl 527
OY 365 GAPIALLVAGVGLIGLIEASQAMFESVYANRLOKRIEMEQNGONGYTFDKYTSRA 424
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 528 asplallvsgltgvtstllgysqamfeyvanklhnklyeweknhnkyfengydaryl 587
OY 425 ATYANLNLKFLSELNKELEAEERVAITQOORNDNIGELAGITTKGERIKSGAKADAFEDG 484
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 588 anlqdmkflnlhnlkelqeeratvlatqgqwdmnlqalagstrlgekvylsgkavdfeeg 647
OY 485 KVEACSNITLDAKTGIIDISNSGKKTQALHETSPLTLAGTESRRLTNGKSYNTKLK 544
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 648 khkacklvgldsaanglidasvnsqkaktqhlfrlpilpgrtehrevqgkyleytlkln 707
OY 545 FGRVKNWQVTDGEASKLDPKSVYIOV-----AETEGTDELGLVYNKAGNDLIFVGQ 597
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 708 ltrvdswkltldgaasctfldtnvqrlgieldnagvntkktckllaklqegddnvfvs 767
OY 598 GKNNIDGGGCHDRFVFSKGGFCNITVDGTSATEAGSYVNRKRVANGDIIYHEVVKQERTK 657
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 768 gteidggeggydtvhystr-gnygalidatketegsgsyvntfvevckalhevtshclal 826
OY 658 VGRRTTIOYRDYELRKVGYGYOSTDNLKSVEEVISOPNDYFKSGKPFNDIFHSGEGDDL 717
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 827 vgnreeklgyr-hsmnqhagyytkdtkaveeeligtsnndlfkgykfkfadafnagsgvdt 885
OY 718 LDGGAADDRLFGCGKNDRLSGDEGDDLDDGSGDDVNLGACGADVITFRKGCNDLTYDG 777
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 886 ldqndgndrlfggkqgdldldgngddfldgkqgndllhggkqgdldfvrhckqgdndlltds 945
OY 778 TGRNDKLAFDANISDIMERTKECIIIVKRNDHSGSINIPRW----ITSNLQWYOSNKTP 833
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 946 dqncklstdsdnklcltfckvknlyl-tnskkekvlqgnwrtfeadfakevpyrkakl-d 1003
OY 834 HKIEQLIGDGSYITSDOIKLIDOKKDGTVITRSOELKRLADENKSQKLSASDIASLNLK 893
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1004 ekeeteligngertsktyqddll--akngskltqgdelskvndyvelklns-krvtnslck 1060
OY 894 LVGSMALFETANSVSSNALQPTOPTQPTG 922
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1061 llsvsafctssndsrnlvaptamlqdsll 1089

```

```

RESULT 3
AAB21073
ID AAB21073 standard; Protein; 1098 AA.
XX
AC AAB21073;
XX
XX 19-DEC-2000 (first entry)
DT
XX Bovine IL-2/Pasteurella haemolytica leukotoxin fusion protein.
DE Bovine IL-2; Interleukin-2; leukotoxin; LKT; respiratory disease;
XX
KW

```

```

KW pneumonia; shipping fever; cattle; livestock; anti-Pasteurella vaccine;
KW immunogen.
XX
XX Chimeric - Bos taurus.
OS Chimeric - Pasteurella haemolytica.
XX
XX US6096320-A.
XX
XX 01-AUG-2000.
XX
XX 20-OCT-1997; 97US-0954418.
XX
XX 20-DEC-1993; 93US-0170126.
XX
XX 22-JUL-1996; 96US-0681479.
PR 22-AUG-1990; 90US-0571301.
PR 16-OCT-1991; 91US-0777715.
XX
XX (UYSA-) UNIV SASKATCHEWAN.
PA (CIBA ) CIBA GEIGY CANADA LTD.
XX
XX Campos M, Hughes HPA, Potter A;
PI
XX WPI; 2000-531543/48.
DR N-PSDB; AAA72483.
XX
XX Vaccine for stimulating immunity against pneumonia comprises chimeric
PT protein comprising gamma-interferon and leukotoxin derived from
XX Pasteurella haemolytica -
XX
XX Example 1; Column 31-38; 56pp; English.
XX
XX The invention relates to a novel vaccine composition comprising an
XX immunogenic chimeric protein that comprises gamma-interferon (gamma-IFN)
XX or an active fragment thereof, linked to an epitope of a Pasteurella
XX haemolytica leukotoxin (LKT). Pasteurella species, especially Pasteurella
XX haemolytica, are responsible for respiratory diseases in a range of
XX agricultural animals, most particularly cattle, but also sheep, pigs,
XX horses and fowl. Shipping fever is the most economically important
XX respiratory disease associated with Pasteurella species, affecting
XX 15-30% of exposed cattle and resulting in a 2-5% mortality rate in the
XX exposed population. The vaccine composition of the invention is
XX is useful for preventing or ameliorating respiratory diseases such as
XX pneumonia, particularly shipping fever pneumonia, in livestock. The
XX present sequence represents a fusion protein comprising bovine
XX interleukin-2 (IL-2) and Pasteurella haemolytica leukotoxin, which may
XX also be used as an anti-Pasteurella vaccine.
XX
XX Sequence 1098 AA;
SQ

```

```

Query Match 50.2%; Score 2334; DB 21; Length 1098;
Best Local Similarity 50.1%; Pred. No. 1,1e-143;
Matches 465; Conservative 175; Mismatches 263; Indels 26; Gaps 13;

```

```

OY 8 KSNIOGLNSTGSKLNLYAIPKD--YDPQKGTLPNDPFIKADDELGIARLAEPNHTT 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 173 gsltqeg-selktcgakklllylpyngydtdegngldvkaaeelgievqreemnat 231
OY 66 AKKSVDTVNOFLSLTQGTGIAISATKLEKFLQKHSTNKLAKGLDVENIDRKLKASNVLS 125
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 232 aqstlgtltaigtalgttergylvlsapqdkllqk---tkagqalgsaesiynanakkatvls 288
OY 126 TLSSFLGTALAGIELDSLIRKGDAPDALAKASIDILINELTGNLSOSTOTIEAFSSQLAK 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 289 gtslilgsvlaqmdleal-qmnsqhalaqkajeltlnsleniansvktldeffgeqisq 347
OY 186 LGSTISQAGFSNIGKNLONL-NFSKTNLGLTITGLSGISGFPALADKNASTGKRVAA 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 348 fgsqkqnlgytlgdklknlgldkaglgldvlsqllsgataalvldaknastakvga 407
OY 245 GFELSNQVIGNVTKAISSVYLAQVAAGLSTTGAVAAALITSSIMLAISPLAFNAAADKFN 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 408 gfeianqvgvnltkavssyllaqgrvaaglsstgvpvaallastcslsplsafagjadtfn 467

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Oy	305	HANHLDEPAKORPKREYDSDHLLAERYOGVGTIANSLTTSTALGAVSAAAGSAV	364
Db	468	haksleyeerfkf.lgydgdlillaeyqrgqlidassva lnralaaiaagysaaaagsvrl	527
Oy	365	GAPIALVLVGVTGLISGLEASKQAMFESVANRLQGIILLEMKGONGONTFDKYDSRYA	424
Db	528	asplallivsgltvgistlllygskgmefhvanklnkiveweknhbknyfengydaryl	587
Oy	425	AYLANNIKFLSELNKLEAEVIATLTQQRWONNIGELGITRKGEERIKSGAVADFEED	484
Db	588	anldmkmkfllnkleigeervataltqqwdnnlgdlaistr lgekvslgkayvdaleeg	647
Oy	485	KKEVAGSNITLDKKTGIIIDISNSNGKTKTQALHFSPBLTLTAETESRERTLNGKSYINLK	544
Db	648	khlkadklvlgdsangllidvnsngkaktcghllfrpbltpgtelnerrvqtokyeytkln	707
Oy	545	FGRVKNMQVTDGEASSKLDESKEYIOHV-----AETEGETDELGVNAKAGNDIRVGO	597
Db	708	invdswkkildgaassffdltnvvqrilgielnaagnvtlkceklilaqlgegddnvrvgs	767
Oy	598	GKNMIDGGDDHDRIFFYSKDGFENITVDGTSATAGSYTVNRKVAKRGDIYEHVKKROETK	657
Db	768	gtteidggdydrvhysr -gnyaltiladtkelegsyrvnr fvetgkalhevsthal	826
Oy	658	VGRTERFTIQRBDVELKRVCYGIOSTNLKSVEEIVGSOPNVFKRSKFENDIFHSGEDDL	717
Db	827	vgnveeklekyr -hsnnqhbagyytkctlkaveellqtsnndlfkskfnndainggdvdt	885
Oy	718	LDCGAGDDRLEFGGKGNRLSGDEGDPLLGGSGSDVLLNGAGANDVYIFRRKDGNDTLXDG	777
Db	886	ldgndgnndrltgygqdilldgngddf idgqknadllbhgkgddflfvnrkdgndllds	945
Oy	778	TGNDKLAFADANISIDMIERTKEGIIYVRKRDHSGSINIRMY----ITSNLÖNQSKNTD	833
Db	946	dgnndlfistsdnldklfekvkhnlyl-tnskkekylgmwfreedfakevpnyark-d	1003
Oy	834	HTEIDLICKDSYITTSDOIKLIQDKKDGTVITISOELKRLADENKSÖQLASDIASSLNK	893
Db	1004	ektieelishqngeritksqvddl-akngnkltcgdeliskrvdynyelikh-kvnensldk	1060
Oy	894	LVGSMALFGTANSVSNNALQPIOTPOGI	922
Db	1061	lissvsaltsndsrdnvlvaptsmlqdsi	1089
RESULT 4			
AAR22103	ID	AAR22103 standard; Protein: 1098 AA.	
XX	AAR22103;		
AC	XX		
DT	XX	06-JUL--1992 (first entry)	
DE	XX	Bovine IL-2 - LRT fusion protein.	
KW	XX	Interleukin 2; leuko-toxin; vaccine; pneumonia; respiratory diseases.	
OS	XX	Pasteurella haemolytica.	
OS	XX	Bos taurus.	
PN	XX	WO9203558-A.	
PD	XX	05-MAR-1992.	
PF	XX	22-AUG-1991; 91WO-CA00299.	
PR	XX	22-AUG-1990; 90US-0571301.	
PA	XX	(POTT/) POTTER A.	
PI	XX	Potter A., Campos M, Hughes HPA.	

XX WP1: 1992-096901/12.
DR N-PSDB: AA022771.
XX Interleukin 2-leuko-toxin gene fusion - encodes fusion protein
XX useful as vaccine for animal pneumonia
XX
XX Claim 20; Fig 3; 68bp; English.
CC The IL-2-IKT protein was encoded by a chimeric gene contg. the
CC bovine IL-2 gene fused to the DNA encoding at least one epitope of
CC leynotoxin from P. haemolytica. IL-2-IKT was gel purified and
CC ligated into the expression vector pGH43 lacI. The resulting
CC clone pAA356 (ATCC 68386) contd. the desired gene fusion under the
CC control of the E. coli lac promoter. The protein produced by the
CC gene fusion is useful in a vaccine compsn. with a pharmaceutically
CC acceptable vehicle, e.g. a carrier homologous to a rotavirus VP6
CC inner capsid protein. The vaccine can be used for preventing or
CC ameliorating respiratory diseases in animals e.g. shipping fever
CC or pneumonia.
CC See also AAR24124,5.
CC
XX
XX Sequence 1098 AA;
SQ

Query Match 50.2%; Score 2332; DB 13; Length 1098;
Best Local Similarity 50.1%; Pred. No. 1,5e+143;
Matches 465; Conservative 174; Mismatches 264; Indels 26; Gaps 13;

8 KSNITQAGLSTKSGKLNLYLAIPKD--YDPKGGTINDEIKAADELGIARLADEPNHET 65
173 qstltvg-selktgakklllyipmqytleqnglqdlivkaeeilyevgrzeennlat 231
66 AKKSVDTVNOFLSLTQTGIAISATKLEKFLQKSTKWLAKGDSYENIDRKAKSNVLS 125
232 agstltqtaigtltgqvlysepqldkllyq--tkagqalgseesivgnankatvls 288
126 TLESFTGATAGLELDSLIKKGDAADALAKASIDLINETIGLMSOSTOTIEAFSSQLAK 185
289 gldslgsvlaqmdleal-qmnsqhalaqagletnslhenlansvktldelgeiqsq 347
186 LGSTISQAKGFNSNGKLNQVL-NFSKTNIGLETITGSLGSLGSAFPLADPNASTGKVVA 244
348 fgsklqniklgtlgtgdklnlkgldkagyltdvisglssatacalyladknastakkyga 407
245 GFELSNQVINVTKALISSYVLAQRYAAGSTGTGAVALITSSIMLAISPLAFNMAADKEN 304
408 gfelangvgnitkavssyllaqrvaaqslstgpyvaallastvslasplafagiadkn 467
305 HANALDEPAKOFKRFYDGHLLAEYRGVGTIEASLITSTALGANVAGVSAAGVAAV 364
468 haksleayaeffkllygdgnlllaeyrgvgtldasvtaintaalaagvsaagavsl 527
365 GAPFALLVAGVYTGISGLIEASKOAMEESVARNLOGKILEMEKONGQONFEDDGYDSRYA 424
528 aspaillvsgtlystcllygskamelehnanklnhtivewekmhbknyfengydaryl 587
425 AYLANNLKFLSELNKELEAERVIAITQORWNNITGELAGITTKGERTKSKAYADAEDG 484
588 anlqdmkflnlhkeiaerviaitlqgwdnnlqdgaisrlgexylsqkaydataleg 647
485 KKEVGSNITTDATKGTITDINSNGKKTQALHPFTSPLLTAGTESRELTNGKYSYINLKL 544
648 khkadeklvqldasnqildvsnaskakqnlitrcplllpgtehnrevvgkgyeklkn 707
545 FGKRVNNOVTOGEASSKLDFSKVIQRY-----AETEGTDEGLIVNAKAGNDIFVQ 597
708 invdswkltdgaasstdclcnvvggrlgeldnagnvltkeltklaklgegdndvfvgs 767
598 GKAMITDGDGHDPRFYSKDGFQGNITVQGTSAATEAGSVTVARKYARQDPIEYVAKROETK 657
768 gteldaggegydlvysr-gnyqyaltdlaktetebegsyvtnrfvetgkahlvevsthtal 826

KW Bovine; Interleukin-2; IL2; P. haemolytica; leukotoxin; LTK;
 KM Ikta; chromosome walking; fusion protein; vaccine;
 KW monoclonal; polyclonal; antibody; ss.
 XX
 OS Pasteurella haemolytica - chimera.
 OS Bos taurus - chimera.
 XX
 PN US5273889-A.
 XX
 PD 28-DEC-1993.
 XX
 PF 22-AUG-1990; 90US-0571301.
 XX
 PR 22-AUG-1990; 90US-0571301.
 PR 16-OCT-1991; 91US-077715.
 XX
 PA (CIBA) CIBA GEIGY CANADA LTD.
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Campos M, Hughes HPA, Potter A;
 XX
 DR WPI; 1994-006687/01.
 DR N-PSDB; AA054212.
 XX
 PT Immunogenic fusion proteins of gamma-interferon and immunogenic
 PT leukotoxin - used in vaccines and to raise monoclonal and polyclonal
 PT antibodies
 XX
 PS Disclosure; Fig 3; 56pp; English.
 XX
 CC This sequence represents a fusion between bovine interleukin-2 (IL2)
 CC and Pasteurella haemolytica leukotoxin (LTK). The leukotoxin gene,
 CC Ikta, was isolated from a gene library of P. haemolytica by
 CC chromosome walking. Immunogenic fusion proteins such as this can be
 CC used in vaccine compositions. It can also be used to raise mono-
 CC and polyclonal antibodies.
 CC
 CC
 SO Sequence 1098 AA;

Query Match 50.1%; Score 2327; DB 15; Length 1098;
 Best Local Similarity 49.9%; Pred. NO. 3.3e-143;
 Matches 464; Conservative 175; Mismatches 264; Indels 26; Gaps 13;
 QY 8 KSNIOAGINSTGKGLKNLYLAIPKD--YDPQKGTLDNFIRADELTARLAEPNHTET 65
 DB 173 gslctag-s-lktgakklllypnyqydtgqnglqdlvkaaeelgveqgreenmat 231
 QY 66 AKRSVDVYNQFLSLTGTGTAISATKLEFLQKHSNKLAKGLDSVENIDKRLGRASNYLS 125
 DB 232 aqtslgtlqtaigterglvlsapqdkllqk---tkagqalgsaesivqnaankakvls 288
 QY 126 TLSSFLGTALAGIELSLIKKGDAPDALAKASIDLINEITGNLSQSTQTEAFSSOLAK 185
 DB 289 gtslslgsvlaagmdldea-qnnsqhnlakagteltsleninsvktldefeqslq 347
 QY 186 LGSTISQAKGFNIGNKLNLT-NFSKTNLEIITLGLSGISAGFALADKNASTGKYAA 244
 DB 348 fsgklnklygltdklnlgldkagjldvlsjlsagtaavl adknaastakvya 407
 QY 245 GFELSNQVIGNWTKAISSVLAQRAVAGSTGTGAVALITSSIMLAISPLAMNADKN 304
 DB 408 gfeiaqvgnaltkavssylaqryvaaglsctgpyvaallastvslajspatajadtfn 467
 QY 305 HANALDEFAKOPRFEGYDGDHLLAEYQGVGTIEASLFTTISTALGAVSAGVSAAVGSAV 364
 DB 468 hakslesyerfkkygdndllaeyqrgtldasvtaintalaaiagvsaaagavl 527
 QY 365 GABIALLVAGVTGLISGILEASKQAMFESVAVNLQGLTLEMEKONGGVYFPKGDSTRYA 424
 DB 528 asplallvsgitvstcllygskamfenvanklnkivewekmhngknyfengydaryl 587
 QY 425 AYLANNLKFLSELNKELEERVAITAOQRMDNNIGELAGITKGERIKSGKAVADAFEDG 484

DB 588 anlqnmkflInlnkelgaervialtqgwdnmgldaglsrlgekylsqayvdafeeg 647
 QY 465 KKEVAGSNITTDAKTGIIIDINSNCKKTOALHFNISPLTATGERERTNKYSYINKLK 544
 DB 648 khikadklvqldasanglidsvnsqakcqnllftrpblpglehervyqtkyeyickln 707
 QY 545 FGKRVKMOVTDGEASSKLDLFSKVIQRV-----AETGTEIGLIYNAKAGNDIYVQ 597
 DB 708 lnrvgswktldgaasftldlnvgrlgldnagnvclkelkllaklgeqddnvtvgs 767
 QY 598 GKMNIIDGDDHVRVYSKDGFGNITTVDTGTSATEGSYTVARKVARGDIYHEVYKRGRTK 657
 DB 768 gtleldggydrvnysr-gnygaltdaeketegqsyvnrivetyalhevsthal 826
 QY 658 VGRKFTIQRDYEELRVGYGYQSTDNLSYEEVIGSQPNDFKSGKNDIFHSGEGDL 717
 DB 827 vnreekleyr-hsmnqhagytkdtklaveeligtshndlfksgkfnndaifngdyvt 885
 QY 718 LDGAGDRLFGSGKGNDRLSGDEDDLDDGSGDDVYLNAGAGNDYIFRKGDGNTLVDG 777
 DB 886 idgndgndplfsgkgddldgngddldgqkgnldllyngygdldlfnrkqgndlctds 945
 QY 778 TGNDKIAFADANISDIMERTEKGIIVKRNDSGSINIPRWY---ITSNLQNYOSKNTD 833
 DB 946 dgncklisdsmkdlftekvhnlvi-tuskkevltlqmwfreadfakevnykatk-d 1003
 QY 834 HKTEQLIGKDSYITSQJIDKTLQDKDGVTTSQELKKLADENKSQKLASDIASSLNLK 893
 DB 1004 ekteeligngerltskyddll--akngkiltqdeliskvvdnyellkhs-kvnsldk 1060
 QY 894 LVGSMALFGTANVSNNALQPTIOPQGI 922
 DB 1061 llsvsafstsdnsrnlvaptsmldqsl 1089
 RESULT 7
 ID AAR42385 standard; protein; 924 AA.
 XX
 AC AAR42385;
 XX
 DT 19-APR-1994 (first entry)
 XX
 DE Recombinant leukotoxin peptide from plasmid pCRR28.
 XX
 KW Haemophilus somnus; immunogenic; haemolysin; lppb; lppc;
 KW thromboembolic meningoencephalitis; septicemia; arthritis;
 KW pneumonia; Ikta gene; haemin-binding protein; fusion protein.
 XX
 OS Pasteurella haemolytica.
 XX
 PN WO9321323-A.
 XX
 PD 28-OCT-1993.
 XX
 PF 05-APR-1993; 93WO-CA00135.
 XX
 PR 09-APR-1992; 92US-0865050.
 PR 04-JUN-1992; 92US-0893424.
 PR 04-JUN-1992; 92US-0893426.
 PR 29-MAR-1993; 93US-0038287.
 PR 29-MAR-1993; 93US-0038288.
 PR 29-MAR-1993; 93US-0038719.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Hatland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
 PI Rioux C, Theisen M;
 XX
 DR WPI; 1993-351733/44.
 DR N-PSDB; AA051086.
 XX

PT Haemophilus somnus immunogenic proteins used in vaccines -
 PT selected from haemin-binding protein, haemolysin, LppB and LppC,
 PT and corresp. DNA

XX Disclosure: Fig 11: 119pp: English.

XX The lppB gene protein was expressed in *E. coli* as a fusion to the
 CC Pasteurella hemolytica leukotoxin gene lktA coded for by plasmid
 CC PA352. The lppB gene fragment was taken from pMS11. LppB can be
 CC used in vaccines for preventing or treating *H. somnus* infections,
 CC which cause thromboembolic meningitis, septicemia, arthritis
 CC and pneumonia in vertebrates.
 CC See also AAR42370-86.

XX Sequence 924 AA:

Query Match 50.1%; Score 2326.5; DB 14; Length 924;
 Best Local Similarity 50.0%; Pred. No. 2,8e-143;
 Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;

QY 15 LNSTKSGKLNLYAIPKD--YDPQKGTLLNDPFAKADDELGIANLAEPNHTFAKKSVD 72
 DB 7 Lstfptkqakkllylpnygydteqngldlvkaaeelqlevqeermlataqtslgt 66
 QY 73 VNQFLSLUTGTIAISATFKLEKFLQKSTNKLAKGLDSVENIDKLGKASNVSLTSLF 132
 DB 67 lqtaigltergavysapglklqk--tkagalgisaeelvanankaktvslqslg 123
 QY 133 TALAGIELDLKKGDAAPDALAKASIDLINELIGNLSOSTQTTEAFSSQLAKGTSIQ 192
 DB 124 svlagndleal-qmnsnqhalakagldeltnslentiansvkldeleglsgfsgklqn 182
 QY 193 AKGFSNIGKNLQNL-NFSKTNLCLEITITGLSGISAKPALADKNASTGKVAAGFELS 251
 DB 183 lkgldglgkklngldkagldgldvsglsgataalvldknaastakkvagfelaq 242
 QY 252 VIGNNVKATSSVYLAQRAVAAGLSTGAVAAALISSIMLISPLAFNMAADKFNHANA 311
 DB 243 vvgnlkavssyllaqrvaaglsstgpaallastvslasplafagldakfnhaksles 302
 QY 312 FAKQFRFGYGDHLLAEYQRGVGTIEASTLTITSTALGANVSAGVSAANAAGCAPIAL 371
 DB 303 yaerfkllgydgdnllaeygrgtldasvtalntalaagvsaagaasvslasplall 362
 QY 372 VAGVTGLISILEASKQAFESVANRLQGIKILEWQKONGQNTFDKGYDSRYAVIAN 431
 DB 363 vsgltgvtislclqyskqamfehvanlklnklveweknngknkfengydarylanldm 422
 QY 432 KPLSELNKELEAEKVIAITQOQBMNNGELAGITTKIGERIKSGKAVADAPEDEK 491
 DB 423 klilnlknlqeeravialclqgwdmnlglaglsrlgexkaysgkaydaeeqknlkadk 482
 QY 492 NITLDARTGIIDISNSNGKTOALHFTSPLTATGESRERLTNGKSYINKLFGRYKM 551
 DB 483 lvgldesangldvsnsgakctqlhlftrplllpgtehrevvqgkyeylklhlnvds 542
 QY 552 QVTNDEASKLDFSKVIQRY-----AETEGDEIGLYNNAKAGNDIVFGCKNIN 604
 DB 543 kltdgaasctfdltnvvgigleldnagnvtckkckklaklgegdhntvfgsgtleidg 602
 QY 605 GDCHDVFVSKDGFNGITVDGTSATEAGSYTVNRKVARDIYHEVYKQRETIVGK 664
 DB 603 gegydvvhysr-gnygalitldackteqgsyvtvrfveqlkalhvtsthalvgnreek 661
 QY 665 IOYRDYELRKVGYSOTDNLKSVREYIGSQFNDVFKSGKFNDFHSGEGDLDLGDG 724
 DB 662 lqeyr-hsnqnhagyytkctlkaveelishndifkgskfndafnggdvctldgndgn 720
 QY 725 DRFGGKGNDRLSGDEGDDLLDGGSDDVLYNGAGNDVYFFRGDGNLTLYDTGNDKLA 784
 DB 721 drlfggkdddlldgngddfdldggkgnldlhggkgnldlfvhrkgdgnldltdsgndkls 780

QY 785 FADANISDIMERTKEGIIVKRNHDHSGINIPRMV-----ITSMQVQSNKTDHKTIO 840
 DB 781 fsdnlkdlitfevkynlly-tnskketvrlqmwfreadakavpykatk-dekteell 838
 QY 841 GKDGSYITSDQIDKILQDKKGTIVTSQELKTLADENKSKSLASDIASSLNKLVGSM 900
 DB 839 gqgerltskqvddll--akngnklqtdelskvndhyellkhs-kvntslklslssvas 895
 QY 901 FGTANSVSSNALOPTITPOPGI 922
 DB 896 fltsndsrnylvaptslmdqsl 917

RESULT 8

AAR42380

ID AAR42380 standard; Protein: 924 AA.

AC AAR42380:

DT 19-APR-1994 (first entry)

XX Recombinant leukotoxin peptide (spllt) from plasmid pCCH4.

XX Haemophilus somnus: immunogenic; haemolysin; LppB; LppC;
 KW thromboembolic meningoencephalitis; septicemia; arthritis;
 KW pneumonia; lktA gene; haemin-binding protein; fusion protein.

OS Pasteurella hemolytica.

PN W09321323-A.

PD 28-OCT-1993.

XX 05-APR-1993; 93WO-CA00135.

XX 09-APR-1992; 92US-0865050.

PR 04-JUN-1992; 92US-0893424.

PR 04-JUN-1992; 92US-0893426.

PR 29-MAR-1993; 93US-0038287.

PR 29-MAR-1993; 93US-0038288.

XX 29-MAR-1993; 93US-0038719.

XX (UYSA-) UNIV SASKATCHEWAN.

PA Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;

PI Rloux C, Theisen M;

DR WPI: 1993-351733/44.

DR N-PSDB: AAO51082.

PT Haemophilus somnus immunogenic proteins used in vaccines -

PT selected from haemin-binding protein, haemolysin, LppB and LppC,

PT and corresp. DNA

XX Disclosure: Fig 6: 119pp: English.

XX The hmb gene encoding the haemin-binding protein was expressed in

CC *E. coli* as a fusion to the Pasteurella hemolytica leukotoxin gene

CC lktA coded for by plasmid PA352. The hmb gene fragment was taken

CC from pRAP504 and starts at the codon for the 33 rd amino acid residue

CC of ORF1. The haemin binding protein can be used in vaccines for

CC preventing or treating *H. somnus* infections, which cause thromboembolic

CC meningoencephalitis, septicemia, arthritis and pneumonia in

CC vertebrates.

CC See also AAR42370-86.

XX Sequence 924 AA:

Query Match 50.1%; Score 2326.5; DB 14; Length 924;
 Best Local Similarity 50.0%; Pred. No. 2,8e-143;
 Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;

OY	15	LNSRKSOLKXNLYAIPMD--YDPQOGSTLWDFIKADEGCEALAEAPHNTFAKSSVOT	72
OY	7	LSfEtqakkiLiLyipgnuyqdtceggngldvikaadeeilyevqeermiaatacsigt	66
OY	73	VNOFELSTQPTAISAARKLEEFLOKHSTNKLAQJOSVENIDBKRLKASNVLTSESPFG	132
Db	67	iqtaigltengivisaagdiqlik---kaagaigsaeetiynankaktvvisqislig	123
OY	133	TALAGIELDSTFKKGDAAPALAKASIDLINETIGNLUSOSTQTTEAFPSOALKGSTISO	192
Db	124	svlagmdideal-qmnsnqhalaekagieltnslteniansvktldeiteglsqfygsklpn	182
OY	193	AKGSNIGNKNQLN-NSKTNMLGLEITTGLLSGISACFALADKNANSTGKKVAAGFLSNQ	251
Db	183	IkgIgtIgdtkInglidkaglidvgtsllgsataalviadknastakkvvaggfelang	242
OY	252	VIGNVTARISSYLAORVAAGLSTTGGVAALLTSIMSILATSPAFMNAAKPFHANAIDE	311
Db	243	vwnghkavssyLIAqvvaaslstcgpvaallaasvaslaSplafgiackImhaksles	302
OY	312	FAKOFKRKEYGDDHLIAEYORGVOTIEASTLTSTIALGAASVASAAAVSAYGAPTALI	371
Db	303	yaeftfkIgyqgdhlIaeeyrgtctidasvatIntaltaiaagsvsaaagsvlaSpiall	362
OY	372	VAGVTGLISGLEAKSKQAMFSVANRLQGKITLEMKGONGONTFDKYDSRYAAYLANNE	431
Db	363	vsqtlgvystlllygskqmtefvhanklnkvewekmhbknykennydarylaanqdm	422
OY	432	KFLSLINKELAENVIAITOORMNNINGELAGTKLEERLKSGAADAEDCKVEAGS	491
Db	423	kflInlnhejaerviatlcgvwdmngdlagistrjexkyslkayydateeikhikadk	482
OY	492	NITTDAKTGIDJISNSNGKTQALHTFTPLTACTESREBLTNGKYSYINKLFGHYKMW	551
Db	483	IvqlidsangliadvensgaktcqhlIftrpllpbttehrevrvgkyeyklkinInvdsW	542
OY	552	OVTQGEASAKLDEFKVIORV-----AETEGDTDELINYAKAAGNDIVPOGKMNIIDG	604
Db	543	kItddaaastfdlinhvyrjieladnaagnvbtkcekklIaklgegddnrvvsgstleIdg	602
OY	605	GGDGHVRVYSKDGFCGNITVGTSATEAGSYTVNRKARYARDIYHEVVAKROEYVFKRTET	664
Db	603	gegydrvyrsr-gnygalatlatcketeegsyvtmrftelgkalhevsthtalvgnreek	661
OY	665	IQYRDYELRKVGYGYOSTDNLSVEEVIYIGSOFNDFVKSGRFNDIFHSBGEDDLIDGAGD	724
Db	662	Ieyr-hsnqnqhagyuktclIkaveeeiligtshndifkyskfndaingogdvdtIdgndgn	720
OY	725	DRLEFGKGNDRLSDEBEGDLLIDGSSGDVYLNGAGNDVYFRKGDGNDTLXDGTGNKLA	784
Db	721	drlIlggkdddIlldgnggdIdlggkgnmlIhgvggadIvnrkvgdnmlIdtsdgunkIs	780
OY	785	PADANISIMIERFEKGIIVKRNHSGSINPRVY----ITSNLQNYSNMKTBIKEOLI	840
Db	781	fdsnlkalketkevkhnlvi-tnskkekvltgmwfreadefakevpykak-dekiell	838
OY	841	GKDGSYITSDOIDKLIDOKDKGVITYTSEOELKLADENKSOKLASASDIASSLNKLVSMAI	900
Db	839	gangetrlsKyvdIdl--akngyklttgelskvvdnyellkhs-kvntnsIdklIssava	895
OY	901	FGTANSVSMMALOPIOTPOGI	922
Db	896	fTsandsrnvlvaptsmdgel	917

RESULT	9
AA42378	
ID	AA42378 standard; protein; 924 AA.
XX	
AC	AA42378;
XX	
DT	19-APR-1994 (first entry)
XX	

DE	Recombinant leukotoxin peptide (splitt) from plasmid pGC5.
XX	
KW	Haemophilus somnus; immunogenic; haemolysin; lppB, lppC;
KW	thromboembolic meningoencephalitis; septicæmia; arthritis;
KW	pneumonia; lktA gene; haemin-binding protein; fusion protein.
XX	
OS	Pasteurella haemolytica.
XX	
PN	W09321323-A.
XX	
PD	28-OCT-1993.
XX	
PE	05-APR-1993; 93WO-CA00135.
XX	
PR	09-APR-1992; 92US-0865050.
PR	04-JUN-1992; 92US-0893424.
PR	04-JUN-1992; 92US-0893426.
PR	29-MAR-1993; 93US-0038287.
PR	29-MAR-1993; 93US-0038288.
PR	29-MAR-1993; 93US-0038719.
XX	
PA	(UYSA-) UNIV SASKATCHEWAN.
XX	
PI	Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
PI	Rioux C, Theisen M;
XX	
DR	WPI; 1993-351733/44.
DR	N-PSDB; AA051081.
XX	
PT	Haemophilus somnus immunogenic proteins used in vaccines -
PT	selected from haemin-binding protein, haemolysin, lppB and lppC,
PT	and corresp. DNA
XX	
PS	Disclosure; Fig 5; 119pp; English.
XX	
CC	The hmb gene encoding the haemin-binding protein was expressed in
CC	E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene
CC	lktA coded for by plasmid pAA352. The hmb gene fragment was taken
CC	from pPA5P01 and starts at the codon for the third amino acid residue
CC	of ORF1. The haemin binding protein can be used in vaccines for
CC	preventing or treating H. somnus infections, which cause thromboembolic
CC	meningo-encephalitis, septicæmia, arthritis and pneumonia in
CC	vertebrates.
CC	See also ARA42370-86.
XX	
SQ	Sequence 924 AA;

	Query Match	50.1%;	Score 3226.5;	DB 14;	Length 924;
	Best Local Similarity	50.0%;	Pred. 2.8e-143;		
	Matches 461;	Conservative 174;	Mismatches 262;	Indels 25;	Gaps 12.
Qy	15 LNSTSGKLNELAIAPKD--YDPOKGGLINDPIKADELGIARLAEHPNHTETAKSVDT	72	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Dd	7 Isfptgakkililylpqnyvdtbegngqgdvlvkaaeeigievgreernistaqtstisgt	66	: :		
Qy	73 VNOPFLSTGTGIAISATKLEKEFLQRHSTNKLAAGSDVENIDRKLGKASNVLTSLSSFG	132	: :		
Dd	67 lqtaqltergerlvislepqdkllqk---lkagaylgseesiivgnankaktviysglisylg	123	: :		
Qy	133 TPLAGIELDSLIRKKGDAAFDALAKKSIDLINELIGNLSOSTTTEAFSSQLAKGSYSISO	192	: :		
Dd	124 svlagndideal-qmnsqhataakagleltmsliaeniansvrltdefgsigfsfkjpn	182	: :		
Qy	193 AKGFNSIGTKLONL-NFSKTNGLETITTLGISISGAPLADKNMSTGCKVAAGELSNO	251	: :		
Dd	183 lkyqltlgqklmhlglidavglidvlsylsgataaalvaldekmasstackvgaagfelang	242	: :		
Qy	252 VIGNVTAKSIVYLQRVAGASTTGGAVALTTSSIMLAISPDLAMNADRNHNNAIADDE	311	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Dd	243 vgnitlkaavssyllaqrvaaqlssrgpvaaallastcvslaisplafatagladckfnhakstes	302	: :		
Qy	312 FAKQPRKFYGDDHLLAEYRGVGTITEASLTITIITALGAVSAVSANAAGVAGPAILL	371	:		

[illegible]

XX comprise sub-unit antigens from P haemolytica fimbrial protein,
Pt plasmin receptor; 50 K outer membrane protein and leukotoxin.
Disclosure: Fig 5; 92pp; English.

CC LTKr352 is 98% homologous with authentic leukotoxin and migrates
Cc to the same position on gels.
CC The LKr352 gene was piped as follows: lktA, an MaeI fragment
cc contg. the gene was ligated into the SmaI site of pUC13 to form
CC pAA179. From this, two constructs were made in the pAc-based
cc vector, pGH412:lact digested with SnaI. One, pAA342, consisted
CC of the 5' AbIII fragment from lktA while the other, pAA345, contained
cC the entire MaeII fragment. Clone pAA342 expressed a truncated
CC leukotoxin peptide at high levels while pAA345 expressed full
CC length leukotoxin at very low levels. The 3' end of the lktA gene
cc of pAA345 was therefore ligated to SV40/BamHI digested pAA342 to
CC yield pAA352 contg. the lkr352 sequence. The protein expressed
CC from the vector can be used to prepare a subunit vaccine with
CC either P. haemolytica antigens, e.g. fimbrial protein, plasmin
CC receptor or 50K outer membrane protein. The vaccines can be used
CC to protect cattle from respiratory diseases such as pneumonia, esp.
CC shipping fever pneumonia.
CC See also AAR14481, 83,84 and 85.

SQ

Sequence 926 AA;

**Query Match 50.1%; Score 2326.5; DB 12; Length 926;
Best Local Similarity 50.0%; Pred. No. 2.8e-143;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12.**

OY 15 LNSTSGKLNLUALPKD--YDPQGCGTLNDPIKADELGIARLAEERNHRETAKRSVDT 72
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 7 lsfpktagakilllypqnyqyvtbegngdqdlvkaeeelgevgreernmlatqtstlgt 66
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 73 VNQLSLTGTGTAISATYLEKFLOKHSTKKLAAGLDSDVENIDRLKGASNVLTSSFLG 132
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 67 iqtaqltergyvlvapqdikllqr---tkaqalgyseesiivqaanekaktvislgislig 123
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 133 TALAGIELDLSKGDADPALAKKSIDLINILTNLSQTITFAFSSQLAKLKISTTSIQ 192
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 124 svlamidmideal-qgnsqnhalakagletnslnleniansvkldelfeqissiqsklqn 182
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 193 AKGFENINKNLONT-NFSKTNGLIEILTIGLSGISAGFPALADRKNASTGRKVVAAGELSNQ 251
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 183 lkgytlctkdalknlmgldkgdiglvdisglvsigatacalvalcknostakkvygaefelnq 242
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 252 VIGNVTDAISSVYLAAQRVAAGLGTTGAVALTISSSIMAISPLAFMNAADRFNHANADE 311
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 243 vvnghitkasvsvylagrvaagsltcpvaallastvaslsplafagladckfhnaksles 302
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 312 FAKORRRKYDGDDHLIAEYGRCVGCTTEASLTITSTRLCAVSAGSVANAAGVAPIALL 371
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 303 yaerfkklxygdndllaeygrtgclidesvtelahtalaiaagyvaaaaasvlaapiall 362
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 372 VAGVTVGLSIGLEASKOAMFESEVNARLRLOCKILEMEKONGONYPPKGVDSRAAVAILANLL 431
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 363 vsfigvavistilglysgkamfehvanlkinkivekemnhgkyfyenygdarylanldgm 422
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 432 KFELSELNELLEARVIATAITOQMNNIGELAGITRKGERIKSGAYADAFFEDCKREVAS 491
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 423 kflinlnkelqgeriyaitlqqwdnnidlaglsrlskevyslqayadafeegkhilkadk 482
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 492 NITTDAAKTGIIDSNSNGKRTOALHFPSPLLTAGRESRBLTNMGYSYINKLKCFGRVKWV 551
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 483 lvglidaangildvensrgakctqhlfifrcplltpgreheerycytyeyltklinlrtdsw 542
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 552 QYTDEASSXSIDESKVVIVRV-----AETGETDIDIGLVNMAKANNDIFVOGGKMNIID 604
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 543 kitdgaaastfcollnvavgigteldnagnvttkeetckilaaklgedcdhvfvysgftcidg 602
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 605 GDGHRVRVFYSKDGGCNTVDGTSATEAGSYVANRKAVIDIHVVNRROETFVKVPKETP 664
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :


```

Db      781 fdsnldkltfckvkhnlv-l-tnskkckvtlqwfreadfakvpyrkatk-dekleeil 838
QY      841 GKGSTYTSDDQIDKILQDKKDGTVITSQELKRLADENKOKSASDIASLKLKLVGSML 900
Db      839 gqggetlckayvddll--akngkltqdeliskvndvyeilkhs-kvtnslidklissvaa 895
QY      901 FGTANSVSSNALOPTPTQPTQGI 922
Db      896 fcsndsrnrvlvaptsmldqsl 917

RESULT 12
AAR50291
ID      AAR50291 standard; Protein; 926 AA.
AC      AAR50291;
XX
XX      06-OCT-1994 (first entry)
XX
XX      Recombinant leukotoxin from plasmid PAA352.
DE
XX      Vaccine: outer membrane protein; OMP; Haemophilus somnus;
KW      Iron regulated protein; leukotoxin; Pasteurella haemolytica;
KW      LKT352.
XX
XX      Pasteurella haemolytica AI (strain B122).
OS
XX      CA2099707-A.
XX
XX      03-JAN-1994.
XX
XX      29-JUN-1993; 93CA-2099707.
XX
XX      02-JUL-1992; 92OS-0908253.
XX
XX      (UYSA-) UNIV SASKATCHEWAN.
XX
XX      Harland RJ, Potter AA;
XX      WPI; 1994-092909/12.
XX      N-PSDB; AAQ44760.
XX
XX      Haemophilus somnus outer membrane protein extract -
PT      enriched with iron-regulated proteins; opt. contg.
XX      Leuco:toxin antigens, for use as vaccine
XX
XX      Claim 5; Fig 5; 78pp; English.
XX
XX      A vaccine comprising an outer membrane protein (OMP) extract of
CC      Haemophilus somnus enriched with iron regulated proteins is new.
CC      The vaccine pref. further comprises an immunogenic leukotoxin
CC      polypeptide, esp. an immunogenic Pasteurella haemolytica leukotoxin
CC      homologous to LKT352. Example 1.2 describes the prodn. of
CC      P. haemolytica recombinant leukotoxin from PAA352.
CC      Two expression constructs were made. One, PAA342, contained the
CC      5' ahail fragment of the ltkA gene, while the other, PAA345,
CC      contained the entire ltkA gene. PAA342 expressed a truncated
CC      leukotoxin peptide at high levels, while PAA345 expressed full
CC      length leukotoxin at very low levels. Therefore, the 3' end
CC      of the ltkA gene was ligated into PAA342, yielding plasmid PAA352.
CC      LKT352 or new leukotoxin is 98% homologous to authentic
CC      leukotoxin.
CC      NB: the protein sequence in Fig 5 comprises 926 amino acids,
CC      however this protein is described in the text as having
CC      931 amino acids.
XX
XX      Sequence 926 AA:
XX
Query Match      50.1%; Score 2326.5; DB 15; Length 926;
Best Local Similarity 50.0%; Pred. No. 2.8e-143;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;
```

```

QY      15 LNSTKSLKNLVLAIPKD--YDPOKCGTLNDFIKADELGIARLAEPPNHTENAKKSVDT 72
Db      7 lsrpctgakkllilylpqnyqydeqnglqdlvkaeeigleqvceermntatacslgyc 66
QY      73 VNQFSLTGTGIAISATKLEKFLQKHSTNKLAKGLDVENIDRKLKASNVLSSTSSFLG 132
Db      67 lqtaigltergvlvlsapqldklilgk---lkagqlgsaeslvgnankaktvlsqslg 123
QY      133 TALAGIELDSLKKGDAADALAKASIDLINELIGLSQSTOTIEAFSSQLAKLGSSTISQ 192
Db      124 svlagmldleal-qmnsnghalakagletnsleniansvktldefigeqsfqsklqn 182
QY      193 AKGFNSNIGKLNLT-NFSKTNIGLEITITGLISGAFALADKNASTGKRVAAFPGLSQ 251
Db      183 lkyglctlgqklknlgldkaglgldvlsqslsgataalvldkhnastakkvagfelanq 242
QY      252 VIGNWTAKAISVYLAQVAAGLSTGAVALAITYSSIMLAISPLAFNMAADKFNHANALDE 311
Db      243 vvgnlckavssylaqgrvaaglsstgvaallaastvslaisplafagldkfnhaksles 302
QY      312 FAKQFRKFGYDGDHLAEYQRCVGTIEASLTITSTALGAVSAGVSAANVAGAVATALL 371
Db      303 yeerfkklygdqnliaeyqrgtldasvtaintalaagvsaagaasvlasplail 362
QY      372 VAGVTGLISGILEASKQAFESVANRLQCKLLEMEKONGONGONFEDKGYDSRYAAYLANNL 431
Db      363 vsqilcgvistllqyskqamfehvanklnklyvekennngknfyengydarylanlqdm 422
QY      432 KFLSELNKELEAEVIAITQQRWNNIGELAGITTKGERIKSGAAVADFEDSKKVEACS 491
Db      423 kfllnlkelqaeervlaigqgwdmnlglaglsrgerkvlsgkayvdefeegkhkhak 482
QY      492 NITLDAKGTGIDISNSNGKKTQALHFTSPLTAGTESREBLTNGKSYTNKLKFGVKKM 551
Db      483 lvgldsaanglfdvsnsgaktqhlfltrpdltpgterhervgkyeyllklnrvdsw 542
QY      552 QWTDGEASSKLDPSKVIQAV-----AETEGDELGLVYNKAGNDLFFVGGKNNING 604
Db      543 kltldgaastfdltlvvgrlgletldnagnvtckekellaklggeddnvfvgsqgtelq 602
QY      605 GDGHDRVFFSKDGFENITVDDTSATEAGSYTVNRKVARAGDIYHEVKKQETVGRKRTET 664
Db      603 geygdtrvhysr-gnygalldatketegsyvtnrfevegkahlvetshtalvgnreek 661
QY      665 IQYRDVELRKVGXYGSTDNLSVEEVIGSQFNDVFKSGKFNDFHSGEDDLLDGGACD 724
Db      662 lcyr-hsnngnhagyytkdtlkaveeligtshndlfkgakfndafngdgvdtdlqndgn 720
QY      725 DRFLGKRGNDRLSGDGDLDLGGSGDDVYLVNGAGNDVYIFRKGDDNPTLYDSTGNDKLA 784
Db      721 drlfggkgddllldgngddfdldgkgnndllhggkgddldfvrkygdndlltdsdyndkls 780
QY      785 FADANSIDMIERTKGGIIVKRNHDHSGSINIPRWY-----ITSNLOWYQSNKTDHKLEOLI 840
Db      781 fdsnldkltfckvkhnlv-l-tnskkckvtlqwfreadfakvpyrkatk-dekleeil 838
QY      841 GKGSTYTSDDQIDKILQDKKDGTVITSQELKRLADENKOKSASDIASLKLKLVGSML 900
Db      839 gqggetlckayvddll--akngkltqdeliskvndvyeilkhs-kvtnslidklissvaa 895
QY      901 FGTANSVSSNALOPTPTQPTQGI 922
Db      896 fcsndsrnrvlvaptsmldqsl 917

RESULT 13
AAR79568
ID      AAR79568 standard; Protein; 926 AA.
XX
XX      AAR79568;
XX
XX      24-DEC-1998 (first entry)
```

XX Leukotoxin 352 polypeptide.
DE
XX Gonadotropin releasing hormone; GnRH; chimera; leukotoxin polypeptide;
KW multimer; vaccine; tumour; Leukotoxin 352; LKT 352; lKtA; plasmid pAA352;
KM cytotoxic.
XX
OS Synthetic.
FH Key location/Qualifiers
FT Misc_feature 11..924
/note="Recombinant Leukotoxin peptide"
XX
XX WO9806848-A1.
XX
XX 19-FEB-1998.
XX
XX 08-AUG-1997; 97WO-CA00559.
XX
XX 09-AUG-1996; 96US-0694865.
XX
XX (UYSA-) UNIV SASKATCHEWAN.
XX
XX Manns JG, Potter AA:
XX WPI: 1998-159540/14.
XX DR N-PSDB; AAV61530.
XX
XX Chimeric protein of leukotoxin and gonadotropin releasing hormone -
PT useful for, e.g. preparation of vaccines for reduction of incidence
PT of mammary tumours in mammals
XX
XX Claim 7; Figure 3.1-9; 118pp; English.
PS
XX The present sequence represents a recombinantly produced or chemically
XX synthesised leukotoxin 352 (LKT 352) polypeptide, derived from the lKtA
XX gene that is present in the plasmid pAA352. This gene produces a
XX truncated protein that has an estimated molecular weight of about 99 kDa
XX and lacks the cytotoxic portion of the molecule. Thus this gene has a
XX higher expression level than that of the full-length molecule. This can
XX be used in the construction of a chimeric protein that comprises a
XX leukotoxin polypeptide, several multimers, and a GnRH sequence. The
XX chimeric protein can be used as a vaccine to help reduce the incidence of
XX mammary tumours in a mammalian individual.
XX
XX Sequence 926 AA:
SQ
Query Match 50.1%; Score 2326.5; DB 19; Length 926;
Best local similarity 50.0%; Pred. No. 2.8e-143;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;
OY 15 LNSTKSGKLNLYAIPKD--YDPOKGTLDNDFIKADEIGIRLAEEPNNHTAKKSVDT 72
DB 7 Lstprkgyakklllylpqnyqydegnqldlvkaaeelgiewgreernitaaatslgt 66
OY 73 VNOFLSTOTGTGIAISATKEKFLQKHSTNKLAKGIDSVENIDRKIKAKSNVLSTSSFLG 132
DB 67 iqtaiglttergvlslspqldklqk---tkagqalgsaesivqnanakaktvlsqslq 123
OY 133 TALAGTFLDSLKKGDAAAPALAKASIDILNETITGNLSSTQRTIEAFSSQLKKGSTISQ 192
DB 124 svlagmldleal-qnsnqhalakagletnslilenlansvkldeifgeqisqfsglqn 182
OY 193 AKGSGNIGNKLOM--NFSKTNLGEITITGLSGISAGFALADKNASTGKVAAGFELSNQ 251
DB 183 ikqlygtldkiknlgldkqgldvlsqllsgataalvlnadnastaktkvvgqfclang 242
OY 252 VIGNVTKAISSYLAQRAAAGLSTTGAAVALITSSIMLAISPLAFMNADKFNHANAALDE 311
DB 243 vvgnlktavssylsqvvaaglsstgprvaalstavlslafagjakinhaksles 302
OY 312 FAKQFRKFGIDGHLAEYRGVGTIEASTITSTALGANVSAGVSAAVGAPITALL 371

DB 303 yaerfkkiygddnlllaeyrgvtgldasvralntalaalagvsaaagsvlasptall 362
OY 372 VAGVTGLISGLEASKOMAFESVANRLQKLTLEEKONGGONVYDKGYDSRYAAYLANNL 431
DB 363 vsigltvstlllygskgmfeivanklnkkivewekmhngkyfemydaaylanldmm 422
OY 432 KFLSELNKELEAERYIALTOORMDNNGELAGITKLERIKSGRAVADAEEDCKRVEAGS 491
DB 423 klllnlnkeiqeervialtqgwdnldlagierlsgekvlsqaydafaeeghlikadk 482
OY 492 NTTLDKAGTIIDISNSNGKTOALHFTSPULTAGRESERLTNGKYSTINKLKGKRYKNW 551
DB 483 lvgldsaangldvsnsgakthqlfltrpiltptgehervqtkyeylftklnlnrtdsw 542
OY 552 QYTDGEASKLDFSKVIVOR-----AETEGTDEIGLIVANAKGNDIDFYGCKMNI 604
DB 543 kildgaastfdlcnvvtqigieldnagnvttkethkllaklgeddncvfvsgttdldg 602
OY 605 GDGHDREVFYSKDGFGNITVDGTSATEAGSYTVNRKVARAGDIYHEVVKROETKGRRET 664
DB 603 gegydrvhysr-gnygalldatketegsylnvrfvetgkhalhevtsthalvgnreek 661
OY 665 IOYRDLELRKVGYGOSTNLTKSVEFVIGSOPFNDFYKSGKFNDFRSGEGDLDLGGAGD 724
DB 662 leyf-hsnqnhagyytkltkaveeiiytsmndlfksgkfndatnggdvtdldgndq 720
OY 725 DRLEFGKGNDRLSGDEGDDLDDGSGDYVLANGANDVYIFPKGNGNTLIDGTNMDKLA 784
DB 721 drifgkgddlldgngddfidgkgnndllhggkqddlfvhhkgqnddlfidsqndkls 780
OY 785 FADANISDIEMERTKEGIIYKRRDHSGINIFRW----ITSNLNYSNKTDRHIEOLI 840
DB 781 fidsnldkltfevknlmlyl-tnskkevtlignvfeadfakevpykatk-dekieeli 838
OY 841 GKDGSYITSPDIDKILDDKKDGTVITISOELKRLADENKSQKLSASDIASSLKLIVGSNA 900
DB 839 gqngerltsgvddll--akngkltqdelstkvndyellkns-kvtnslklissvsa 895
OY 901 FGTAHSVSNALQPTIQPTQGI 922
DB 896 ftsdsdnrvlaptlmdqsl 917
RESULT 14
AAW03942
ID AAW03942 standard; Protein; 977 AA.
XX
XX AAW03942;
AC
XX
DT 20-NOV-1996 (first entry)
XX
XX LKT-GnRH protein fusion from pCB113.
DE
XX Leukotoxin; LKT; gonadotropin-releasing hormone; GnRH;
KW fusion protein; immunogen; vaccine; fertility control;
KW contraceptive; sterilisation.
XX
OS Chimeric Pasteurella haemolytica A1 strain B122;
OS Chimeric synthetic.
XX
FH Key location/Qualifiers
FT Domain 1..929
FT Domain /label= LKT
FT Domain 927..977
FT Domain /label= GnRH_repeat_domain
XX
XX W09624675-A1.
XX
XX 15-AUG-1996.
XX
XX 24-JAN-1996; 96WO-CA00049.
XX

[illegible]

RESULT	15
AAW79569	
ID	AAW79569 standard; Protein: 977 AA.
XX	
AC	
XX	AAW79569;
DT	24-DEC-1998 (first entry)

DE	LKT-GnRH chimeric protein.
XX	
KW	Chimera; PCB113; LKT 352; GnRH; Gonadotropin releasing hormone; multimer;
KW	cytotoxic activity; antigen presentation; immune response; vaccine;
KW	tumour.
XX	
OS	Synthetic.
XX	
PN	WO9806848-A1.
PD	19-FEB-1998.
XX	
PF	08-AUG-1997; 97WO-CA00559.
XX	
PR	09-AUG-1996; 96US-0694865.
XX	
PA	(UUSA-) UNIV SASKATCHEWAN.
PI	
PI	Manns JG, Potter AA;
XX	
DR	WPI; 1998-159540/14.
DR	N-PSDB; AAV61531.
XX	
XX	Chimeric protein of leukotoxin and gonadotropin releasing hormone -
PT	useful for, e.g. preparation of vaccines for reduction of incidence
PT	of mammary tumours in mammals
XX	
PS	Disclosure; Figure 5.1-8; 118pp; English.
XX	
CC	The present sequence represents the LKT-GnRH chimeric protein from
CC	PCB113. This plasmid contains the LKT 352 polypeptide (AAW79568) fused
CC	to four copies of the GnRH peptide. This chimera lacks cytotoxic
CC	activity which enables there to be an increase in antigen presentation
CC	and thus an optimal immune response. The removal of this region also
CC	enables the truncated LKT to be expressed at much higher levels and
CC	allows the amount of antigen administered to be reduced. This chimeric
CC	protein comprises a leukotoxin polypeptide, several multimers, and a GnRH
CC	sequence. The chimeric protein can be used as a vaccine to help reduce
CC	the incidence of mammary tumours in a mammalian individual.

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OM protein - protein search, using sw model

Run on: September 11, 2002, 09:01:54 : Search time 22.74 Seconds
(without alignments)
20.432 Million cell updates/sec

Title: US-09-884-696-6
Perfect score: 57

Sequence: 1 FLSELINKLEAE 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	75.4	953	LKAI_PASHA	P16535 pasteurella
2	43	75.4	953	LKAI_PASHA	P55116 pasteurella
3	43	75.4	953	LKAI_PASHA	P55118 pasteurella
4	43	75.4	953	LKAI_PASHA	P55117 pasteurella
5	43	75.4	956	HLVA_PASHA	000991 actinobacil
6	43	75.4	956	RT2A_ACTPL	P15377 actinobacil
7	39	68.4	338	FLIG_BACSU	F23448 bacillus su
8	39	68.4	454	NFM_PIG	P08552 sus scrofa
9	39	68.4	810	NFM_BOVIN	O77788 bos taurus
10	39	68.4	845	NFM_MOUSE	P12839 rattus norv
11	39	68.4	845	NFM_MOUSE	P08553 mus musculu
12	39	68.4	857	NFM_CHICK	P16053 gallus gall
13	39	68.4	915	NFM_HUMAN	P07197 homo sapien
14	39	68.4	947	LKTA_PASP	P55123 pasteurella
15	38	66.7	181	YE18_METJA	O58813 methanococ
16	37	64.9	343	HRCA_BACSH	O69266 bacillus sp
17	37	64.9	356	BASS_SALTY	P36557 salmonella
18	37	64.9	363	BASS_ECOLI	P30844 escherichia
19	37	64.9	663	YD58_YEAST	O03281 saccharomyc
20	37	64.9	699	TOPI_FERIS	O34204 feriyidobact
21	36.5	63.2	617	YE33_AQVAE	O67448 aquifex aeo
22	36	63.2	378	HGDB_ACTFE	P11570 acidamino
23	36	63.2	557	THS2_HALVO	O30560 halobacteri
24	36	63.2	828	YFMA_YEAST	P43555 saccharomyc
25	36	63.2	3321	KEND_HUMAN	O93561 homo sapien
26	35	61.4	163	ATPX_OCHNE	O40608 ochrosphaer
27	35	61.4	207	ATPE_MYCPN	O50377 mycoplasma
28	35	61.4	264	HRCA_CAMJE	O9P982 campylobact
29	35	61.4	445	PREA_BACTU	P10025 bacillus th
30	35	61.4	455	MYH6_RABIT	P04460 oryctolagus
31	35	61.4	468	IFET_CRLO	O60462 cricetus
32	35	61.4	579	G160_HUMAN	O08378 homo sapien
33	35	61.4	621	LAMC_DROME	O03427 drosophila

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	953 AA.
LKAI_PASHA				
ID	LKAI_PASHA			
AC	P16535:			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Leukotoxin from serotype A1.			
GN	LKTA.			
OS	Pasteurella haemolytica.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;			
OC	Mannheimia.			
OX	NCBI_TaxID=75985;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-SEROTYPE A1 / PHL101;			
RX	MEDLINE=69210283; PubMed=2707120;			
RA	Highlander S.K., Chidambaram M., Engler M.J., Weinstein G.M.;			
RT	"DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster".;			
RT	DNA 8:15-28(1989).			
RL	[3]			
RN	SEQUENCE OF 884-953 FROM N.A.			
RP	STRAIN-SEROTYPE A1 / PHL101;			
RX	MEDLINE=90236888; PubMed=2185213;			
RA	Highlander S.K., Engler M.J., Weinstein G.M.;			
RT	"Secretion and expression of the Pasteurella haemolytica leukotoxin.";			
RT	J. Bacteriol. 172:2343-2350(1990).			
RL	[1]			
RN	FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- DOMAIN: THE GUY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY.			
CC	- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).			
CC	- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN MODIFIED (BY SIMILARITY).			
CC	- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.			
CC	-----			
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34	35	61.4	736	1	MYH7_RABIT	P04461 oryctolagus
35	35	61.4	1102	1	MYSC_CHICK	P29616 gallus gall
36	35	61.4	1325	1	G160_MOUSE	P55937 mus musculu
37	35	61.4	1934	1	MYH7_MESAU	P13540 mesocricetu
38	35	61.4	1935	1	MYH7_PIG	P79293 sus scrofa
39	35	61.4	1935	1	MYH7_RAT	P02564 rattus norv
40	35	61.4	1938	1	MYH6_MOUSE	O02566 mus musculu
41	35	61.4	1938	1	MYH6_RAT	P02563 rattus norv
42	35	61.4	1938	1	MYH6_AEOR	P24773 aequipecten
43	35	61.4	1939	1	MYH6_HUMAN	P13533 homo sapien
44	35	61.4	1939	1	MYH6_MESAU	P13539 mesocricetu
45	34	59.6	39	1	EXE3_HEILHO	P20394 heloderma h

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CC -----
DR EMBL: U01216; AAB36691.1; -.
DR HSSP: P02392; ICTP.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RTX_A.
DR Pfam: PF00353; hemolysinCabin; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CARNINGRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 2.
KW Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
KW Transmembrane; Lipoprotein; Palmitate.
FT TRANSMEM 229 249 POTENTIAL.
FT TRANSMEM 297 318 POTENTIAL.
FT TRANSMEM 381 401 POTENTIAL.
FT DOMAIN 734 784 6 X REPEATS, GLY-RICH.
FT REPEAT 734 739 1.
FT REPEAT 743 748 2.
FT REPEAT 752 757 3.
FT REPEAT 761 766 4.
FT REPEAT 770 775 5.

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FT REPEAT 779 /84 0. FDBDCE2FDC85FDF2 CRC64;
SQ SEQUENCE 953 AA; 101948 MW; 101948 MW; 101948 MW; 101948 MW;

Query Match 75.4%; Score 43; DB 1; Length 953;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0.

OY 1 FLSELNKLEAE 12
    || |||||:|
DB 451 FLINLNKLEQAE 462

RESULT 3
LKAB_PASHA
ID LKAB_PASHA STANDARD; PRT; 953 AA.
AC P55118;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Leukotoxin from serotype All.
LN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimella.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SEROTYPE All;
RX MEDLINE=94041617; PubMed=8225575;
RT Burrows L.V., Olan-Wainfield E., Lo R.Y.C.;
RA "Molecular analysis of the leukotoxin determinants from Pasteurella
RL haemolytica serotypes 1 to 16."
RL Infect. Immun. 61:5001-5007(1993).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN

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CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC or send an email to license@isb-slb.ch).
CC -----
CC EMBL: 001215; AAB36689.1; -
CC InterPro: IPR001343; Hemlysn_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC InterPro: IPR003995; RTX_N.
CC Pfam: PF00353; hemolysinCbind; 1.
CC Pfam: PF02382; RTX; 1.
CC PRINTS: PR00313; CABDNGRPT.
CC PRINTS: PR01488; RTXTOXINA.
CC PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4.
CC Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; palmitate.
CC TRANSMEM 230 250 POTENTIAL.
CC TRANSMEM 297 317 POTENTIAL.
CC TRANSMEM 381 401 POTENTIAL.
CC DOMAIN 734 784 6 X REPEATS, GLY-RICH.
CC REPEAT 734 739 1.
CC REPEAT 743 748 2.
CC REPEAT 752 757 3.
CC REPEAT 761 766 4.
CC REPEAT 770 775 5.
CC REPEAT 779 784 6.
SQ SEQUENCE 953 AA: 102206 MW: 927FF56CFC884F12 CXC64;

Query Match 75.4%; Score 43; DB 1; Length 953;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSLNKLELAE 12
DB 451 FLNLNKLQAE 462
II IIIII:II
LRAA_PASHA STANDARD; PRT; 955 AA.
ID LRAA_PASHA STANDARD; PRT; 955 AA.
AC P55117;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Leukotoxin from serotype T10.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROTYPE T10;
RC MEDLINE=96425875; PubMed=8828217;
RA Lathson F.A., Murray J., Davies R.C., Donachie W.;
RT "Characterization of epitopes involved in the neutralization of
RT Pasteurella haemolytica serotype A1 leukotoxin.";
RL Microbiology 142:2499-2507(1996).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE

CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC or send an email to license@isb-slb.ch).
CC -----
CC EMBL: Z26247; CAA81206.1; -
CC InterPro: IPR001343; Hemlysn_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC InterPro: IPR003995; RTX_N.
CC Pfam: PF00353; hemolysinCbind; 1.
CC Pfam: PF02382; RTX; 1.
CC PRINTS: PR00313; CABDNGRPT.
CC PRINTS: PR01488; RTXTOXINA.
CC PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4.
CC Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; palmitate.
CC TRANSMEM 299 319 POTENTIAL.
CC TRANSMEM 361 381 POTENTIAL.
CC TRANSMEM 383 403 POTENTIAL.
CC DOMAIN 736 786 6 X REPEATS, GLY-RICH.
CC REPEAT 736 741 1.
CC REPEAT 745 750 2.
CC REPEAT 754 759 3.
CC REPEAT 763 768 4.
CC REPEAT 772 777 5.
CC REPEAT 781 786 6.
SQ SEQUENCE 955 AA: 102187 MW: B60F2DB8168BECAC CXC64;

Query Match 75.4%; Score 43; DB 1; Length 955;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSLNKLELAE 12
DB 453 FLNLNKLQAE 464
II IIIII:II
HLVA_ACTSU STANDARD; PRT; 956 AA.
ID HLVA_ACTSU STANDARD; PRT; 956 AA.
AC 000951;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Hemolysin (Cytolysin II) (CLY-IIA) (CYTC) (APPA).
GN APPA OR CLYIIA OR HLVIYA OR CYTC.
OS Actinobacillus suis.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OX NCBI_TaxID=716;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3714;
RC MEDLINE=92267623; PubMed=1587585;
RA Burrows L.V., Lo R.Y.;
RT "Molecular characterization of an RTX toxin determinant from
RT Actinobacillus suis.";
RL Infect. Immun. 60:2166-2173(1992).
CC -1- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.SUIS. MIGHT BE A
CC SECRETED CYTOTOXIN, POSSIBLY THE EXTRACELLULAR HEMOLYSIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.

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CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M90440; AAA21918.1; -.
CC InterPro: IPR001343; Hemlysn_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC InterPro: IPR003995; RCXA.
CC Pfam: PF00353; hemolysincabind; 1.
CC Pfam: PF02382; RTX; 1.
CC PRINTS: PR00313; CABNDNGRPT.
CC PRINTS: PR01488; RTXTOXINA.
CC PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 1.
CC Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; Palmitate.
CC TRANSMEM 238 254 POTENTIAL.
CC TRANSMEM 302 320 POTENTIAL.
CC DOMAIN 383 406 POTENTIAL.
CC REPEAT 719 799 9 X REPEATS, GLY-RICH.
CC REPEAT 719 724 1.
CC REPEAT 728 733 2.
CC REPEAT 737 742 3.
CC REPEAT 746 751 4.
CC REPEAT 755 760 5.
CC REPEAT 773 778 6.
CC REPEAT 782 787 7.
CC REPEAT 794 799 8.
CC REPEAT 956 102453 3415FE1D7ADD4365 CRC64;
CC SEQUENCE
OY 1 FLSLNKLELAE 12
Db 455 FLINLNKELOAE 466

Query Match 75.4%; Score 43; DB 1; Length 956;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 9; Conservative 1; Mismatches 0; Gaps 0;

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RP SEQUENCE FROM N.A.
RC STRAIN-ISOLATE CVI 13261 / SEROTYPE 9;
RX MEDLINE=92040145; PubMed=1937809;
RA Smith M.A., Britaire J., Jansen R., Smith H.E., Kamp E.M.,
RA Gielkens A.L.,
RT "Cytolysins of Actinobacillus pleuropneumoniae serotype 9.",
RL Infect. Immun. 59:4497-4504(1991).
CC -1- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.PLEUROPNEUMONIAE,
CC WHICH SHOWS A WEAK HEMOLYTIC ACTIVITY AND IS MODERATELY CYTOTOXIC
CC FOR ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY (BY SIMILARITY).
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PTM: PALMITOYLATED BY APXIC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC -----
CC EMBL: M30602; AAA87232.1; -.
CC EMBL: X61111; CAA43423.1; -.
CC PIR: B33389; B33389.
CC PIR: S18853; S18853.
CC InterPro: IPR001343; Hemlysn_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC InterPro: IPR003995; RCXA.
CC Pfam: PF00353; hemolysincabind; 1.
CC Pfam: PF02382; RTX; 1.
CC PRINTS: PR00313; CABNDNGRPT.
CC PRINTS: PR01488; RTXTOXINA.
CC PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 1.
CC Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; Palmitate.
CC TRANSMEM 233 256 POTENTIAL.
CC TRANSMEM 266 323 POTENTIAL.
CC TRANSMEM 361 406 POTENTIAL.
CC DOMAIN 719 787 8 X REPEATS, GLY-RICH.
CC REPEAT 719 724 1.
CC REPEAT 728 733 2.
CC REPEAT 737 742 3.
CC REPEAT 746 751 4.
CC REPEAT 755 760 5.
CC REPEAT 773 778 6.
CC REPEAT 782 787 7.
CC REPEAT 787 794 8.
CC SEQUENCE 956 AA; 102531 MW; BDBCABRADF1A641 CRC64;
OY 1 FLSLNKLELAE 12
Db 455 FLINLNKELOAE 466

Query Match 75.4%; Score 43; DB 1; Length 956;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

DE Flagellar motor switch protein flig.
GN flig.
OC Bacillus subtilis.
OC Bacillus/Firmicutes; Bacillus/Clostridium group;
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=91258343; PubMed=1828465;
RA Albertini A.M., Caramori T., Crabli W.D., Scoffone F., Galizzi A.;
RT "The fla locus of Bacillus subtilis is part of a large operon coding
for flagellar structures, motility functions, and an Arpase-like
polypeptide."
RL J. Bacteriol. 173:3573-3579(1991).
CC -1- FUNCTION: ONE OF THE PROTEINS THAT FORM A SWITCH COMPLEX THAT IS
PROPOSED TO BE LOCATED AT THE BASE OF THE BASAL BODY. THIS COMPLEX
INTERACTS WITH CHEMOTAXIS PROTEINS (SUCH AS CHEY) IN ADDITION TO
CONTRACTING COMPONENTS OF THE MOTOR THAT DETERMINE THE DIRECTION OF
FLAGELLAR ROTATION.
CC -1- SUBCELLULAR LOCATION: Membrane-associated (by similarity).
CC -1- SIMILARITY: BELONGS TO THE FLIG FAMILY.
CC -----
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CC -----
DR EMBL: X56049; CAA39521.1; -
DR EMBL: 299112; CAB13495.1; -
DR PIR: S14495; S14495.
DR PIR: B42365; B42365.
DR HSSP: Q9WY63; 1QC7.
DR Subtilist; BG10241; flig.
DR InterPro: IPR000090; Flg_Motor_Flg.
DR Pfam: PF01706; Flg-C_1
DR PRINTS: PR00934; FLGMOTORFLIG.
DR Chemotaxis; Flagella; Flagellar rotation; Membrane; Complete proteome.
SQ SEQUENCE 338 AA; 38191 MW; 8C44193BA0ADE58E CRC64;

Query Match 68.4%; Score 39; DB 1; Length 338;
Best Local Similarity 72.7%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 LSELNKELEAE 12
||||| :|||
Db 150 LSELNKEVQAE 160

RESULT 8
ID NFM_PIG STANDARD; PRT; 454 AA.
AC P08552;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurofilament triplet M protein (160 kDa neurofilament protein)
DE (Neurofilament medium polypeptide) (NF-M) (Fragment).
DE NEF3 OR NEFM.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP TISSUE=Spinal cord;
RC MEDLINE=85076594; PubMed=6439558;
RX Geisler N., Fischer S., Vandekeckhove J., Plessmann U., Weber K.;
RT "Hybrid character of a large neurofilament protein (NF-M):

RT Intermediate filament type sequence followed by a long and acidic
carboxy-terminal extension."
RL EMBL J. 3:2701-2706(1984).
CC -1- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
CC -1- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P. NFM IS
PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
THOUGHT THAT PHOSPHORYLATION OF NFM RESULTS IN THE FORMATION OF
INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
OF AXONAL CALIBER.
CC -1- PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H). THE
LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
DR PIR: A03075; ORPDM.
DR InterPro: IPR001664; IF.
DR Pfam: PF00038; filament; 1.
DR PROSITE: PS00226; IF; 1.
KW Intermediate filament; Collod coll; Neurone; Acetylation;
KW Phosphorylation; Glycoprotein.
FT MOD_RES 1
FT DOMAIN 1 104
FT FT 105 412
FT DOMAIN 413 >454
FT FT 105 136
FT DOMAIN 137 149
FT FT 150 248
FT DOMAIN 249 265
FT FT 266 287
FT DOMAIN 288 291
FT FT 292 411
FT FT 412 47
FT CARBOHYD 432
FT CARBOHYD 454
FT NON_TER 454
SQ SEQUENCE 454 AA; 51854 MW; C809282E9C903A6B CRC64;

Query Match 68.4%; Score 39; DB 1; Length 454;
Best Local Similarity 58.3%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSLNKELEAE 12
:|: |||:|
Db 121 YLEQNKELIEAE 132

RESULT 9
ID NFM_BOVIN STANDARD; PRT; 810 AA.
AC O7788;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurofilament triplet M protein (160 kDa neurofilament protein)
DE (Neurofilament medium polypeptide) (NF-M) (Fragment).
DE NEF3 OR NEFM OR NFM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Hill W.D., Zhang L., Ballin B.J., Sprinkle T.J., Spicer K.,
RA Gearhart D.A.;
RT "The bovine neurofilament M subunit has a novel set of KSP repeats
normally restricted to NF-H."
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
CC -1- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P. NFM IS
PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS

Query Match 68.4%; Score 39; DB 1; Length 845;
 Best Local Similarity 58.3%; Pred. No. 39;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLESLNKELEAE 12
 : | : | | : | | |
 DB 119 YLEQONKEIEAE 130

RESULT 11

NFM_MOUSE STANDARD; PRT; 848 AA.
 ID NFM_MOUSE 061961;
 AC P08553; 061961;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neurofilament triplet M protein (160 kDa neurofilament protein)
 DE (Neurofilament medium polypeptide) (NF-M).
 GN NEF3 OR NFM OR NFM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8724694; PubMed=3036526;
 RA Levy E., Liem R.K.H., D'Eustachio P., Cowan N.J.;
 RT "Structure and evolutionary origin of the gene encoding mouse NF-M,
 RL the middle-molecular-mass neurofilament protein.";
 RL Eur. J. Biochem. 166:71-77(1987).
 RN [2]
 RP SEQUENCE OF 322-540 FROM N.A.
 RX MEDLINE=8715837; PubMed=3103956;
 RA Julien J.-P., Meyer D., Flavell D., Hurst J., Grosved F.;
 RT "Cloning and developmental expression of the murine neurofilament
 RL gene family.";
 RL Brain Res. 387:243-250(1986).
 CC -1- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
 CC AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
 CC -1- PFM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS
 CC PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
 CC THOUGHT THAT PHOSPHORYLATION OF NEF RESULTS IN THE FORMATION OF
 CC INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
 CC OF AXONAL CALIBER.
 CC -1- PFM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
 CC OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE
 CC LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
 CC COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
 CC -1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
 CC -----
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 CC -----
 CC EMBL; X05640; CAA29127.1; -;
 DR EMBL; M20481; AAA39815.1; -;
 DR PIR; S00030; S00030.
 DR MGD; MGI:97314; Nfm.
 DR InterPro; IPR001664; IF.
 DR Pfam; PF00038; Filament; 1.
 DR PROSITE; PS00226; IF; 1.
 KW Intermediate filament; Coiled coil; Neurone; Phosphorylation;
 KW Glycoprotein.
 FT INIT_MET 0
 FT DOMAIN 1 102 HEAD.
 FT DOMAIN 103 410 ROD.
 FT DOMAIN 411 848 TAIL.

FT DOMAIN 103 134 COIL 1A.
 FT DOMAIN 135 147 LINKER 1.
 FT DOMAIN 148 246 COIL 1B.
 FT DOMAIN 247 263 LINKER 12.
 FT DOMAIN 264 285 COIL 2A.
 FT DOMAIN 286 289 LINKER 2.
 FT DOMAIN 290 410 COIL 2B.
 FT CARBOHYD 47 47 O-LINKED (GLCNAC) (BY SIMILARITY).
 FT CARBOHYD 430 430 O-LINKED (GLCNAC) (BY SIMILARITY).
 FT CONFLICT 432 432 S -> F (IN REF. 2).
 FT CONFLICT 539 540 QA -> RR (IN REF. 2).
 SQ SEQUENCE 848 AA; 95910 MW; 5F251F274D0F13B6 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 848;
 Best Local Similarity 58.3%; Pred. No. 39;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLESLNKELEAE 12
 : | : | | : | | |
 DB 119 YLEQONKEIEAE 130

RESULT 12

NFM_CHICK STANDARD; PRT; 857 AA.
 ID NFM_CHICK
 AC P16053;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neurofilament triplet M protein (160 kDa neurofilament protein)
 DE (Neurofilament medium polypeptide) (NF-M).
 GN NFM.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90174973; PubMed=2106668;
 RA Zopf D., Dineva B., Betz H., Gundelfinger E.D.;
 RT "Isolation of the chicken middle-molecular weight neurofilament
 RL (NF-M) gene and characterization of its promoter.";
 RL Nucleic Acids Res. 18:521-529(1990).
 RN [2]
 RP SEQUENCE OF 259-857 FROM N.A.
 RX MEDLINE=88112814; PubMed=3123320;
 RA Zopf D., Hermans-Borgmeyer I., Gundelfinger E.D., Betz H.;
 RT "Identification of gene products expressed in the developing chick
 RL visual system: characterization of a middle-molecular-weight
 RL neurofilament cDNA.";
 RL Genes Dev. 1:699-708(1987).
 CC -1- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
 CC AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
 CC -1- PFM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS
 CC PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
 CC THOUGHT THAT PHOSPHORYLATION OF NEF RESULTS IN THE FORMATION OF
 CC INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
 CC OF AXONAL CALIBER.
 CC -1- PFM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
 CC OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE
 CC LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
 CC COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
 CC -1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
 CC -----
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 CC -----

CC EMBL: X17102; CAA34958.1; -
 DR EMBL: X05558; CAA29073.1; -
 DR PIR: A27040; A27040.
 DR PIR: S08061; S08061.
 DR PIR: S15762; S15762.
 DR InterPro: IPR001664; IF.
 DR Pfam: PF00038; filament; 1.
 DR PROSITE: PS00226; IF; 1.
 KW Intermediate filament; Coiled coil; Neurone; Phosphorylation;
 Glycoprotein.
 FT INIT_MET 0
 FT DOMAIN 1 98 HEAD.
 FT DOMAIN 99 406 ROD.
 FT DOMAIN 407 857 TAIL.
 FT DOMAIN 99 130 COIL 1A.
 FT DOMAIN 131 143 COIL 1.
 FT DOMAIN 144 242 COIL 1B.
 FT DOMAIN 243 259 LINKER 12.
 FT DOMAIN 260 281 COIL 2A.
 FT DOMAIN 282 285 LINKER 2.
 FT DOMAIN 286 406 COIL 2B.
 FT CARBOHYD 46 46 O-LINKED (GLCNAC) (BY SIMILARITY).
 FT CARBOHYD 426 426 O-LINKED (GLCNAC) (BY SIMILARITY).
 FT CONFLICT 546 546 G -> R (IN REF. 2).
 SQ SEQUENCE 857 AA; 95704 MW; 4E2E0FC6AC64778B CRC64;

Query Match 68.4%; Score 39; DB 1; Length 857;
 Best Local Similarity 58.3%; Pred. No. 40;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSEINKLEAE 12
 Db 115 YLEQNKKEIEAE 126

RESULT 13
 NFM_HUMAN STANDARD; PRT; 915 AA.
 ID NFM_HUMAN
 AC P07197;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neurofilament triplet M protein (160 kDa neurofilament protein)
 DE (Neurofilament medium polypeptide) (NF-M) (Neurofilament 3).
 GN NEF3 OR NFM OR NFM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 OX [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=87275853; PubMed=3608989;
 RA Myers M.W., Lazzarini R.A., Lee V.M.-Y., Schlepfer W.W., Nelson D.L.;
 RT "The human mid-size neurofilament subunit: a repeated protein
 RT sequence and the relationship of its gene to the intermediate
 RT filament gene family."
 RL EMBO J. 6:1617-1626(1987).
 RN [2]
 RP SEQUENCE OF ONE OF THE 13 RESIDUE REPEATS.
 RX MEDLINE=88158120; PubMed=2450354;
 RA Lee V.M.-Y., Olivos L. Jr., Carden M.J., Hollosi M., Dietzschold B.,
 RA Lazzarini R.A.;
 RT "Identification of the major multiphosphorylation site in mammalian
 RT neurofilaments."
 RL CC -I- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
 CC AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
 CC -I- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P. NFM IS
 CC PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
 CC THOUGHT THAT PHOSPHORYLATION OF NFM RESULTS IN THE MAINTENANCE
 CC INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE

CC OF AXONAL CALIBER.
 CC -I- PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
 CC OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE
 CC LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
 CC COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
 CC -I- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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 CC
 CC EMBL: Y00067; CAA68276.1; -
 DR PIR: A27864; A27864.
 DR PIR: A30157; A30157.
 DR MIM: 162250; -
 DR InterPro: IPR001664; IF.
 DR Pfam: PF00038; filament; 1.
 DR PROSITE: PS00226; IF; 1.
 KW Intermediate filament; Coiled coil; Neurone; Phosphorylation;
 Glycoprotein.
 FT INIT_MET 0
 FT DOMAIN 1 103 HEAD.
 FT DOMAIN 104 411 ROD.
 FT DOMAIN 412 915 TAIL.
 FT DOMAIN 104 135 COIL 1A.
 FT DOMAIN 136 148 LINKER 1.
 FT DOMAIN 149 247 COIL 1B.
 FT DOMAIN 248 264 LINKER 12.
 FT DOMAIN 265 286 COIL 2A.
 FT DOMAIN 287 290 LINKER 2.
 FT DOMAIN 291 411 COIL 2B.
 FT DOMAIN 613 690 6 X 13 AA TANDEM REPEATS.
 FT CARBOHYD 46 46 O-LINKED (GLCNAC) (BY SIMILARITY).
 FT CARBOHYD 430 430 O-LINKED (GLCNAC) (BY SIMILARITY).
 SQ SEQUENCE 915 AA; 102317 MW; 5F5D3DF34C9D9E50 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 915;
 Best Local Similarity 58.3%; Pred. No. 43;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSEINKLEAE 12
 Db 120 YLEQNKKEIEAE 131

RESULT 14
 LKTA_PASSP STANDARD; PRT; 947 AA.
 ID LKTA_PASSP
 AC P55123;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Leukotoxin.
 GN LKTA.
 OS Pasteurella haemolytica-like sp. (strain 5943B).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Pasteurella
 OX NCBI_TaxID=28165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93239320; PubMed=8478098;
 RA Chang Y.-F., Ma D.-P., Shi J., Chengappa M.M.;
 RT "Molecular characterization of a leukotoxin gene from a Pasteurella
 RT haemolytica-like organism, encoding a new member of the RTX toxin
 RT family."
 RL Infect. Immun. 61:2089-2095(1993).
 CC -I- FUNCTION: VIRULENCE FACTOR WHICH IS CYTOTOXIC FOR LEUKOCYTES BUT
 CC IS NOT HEMOLYTIC.


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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PFM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC -----
CC EMBL: L12148; AAA16444.1; -.
CC InterPro: IPR001343; Hemlysn_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC Pfam: PF00353; hemolysinCbind; 1.
CC DR Pfam: PF02382; RTX; 1.
CC DR PRINTS: PR00313; CABNDNGRPT.
CC DR PRINTS: PR01488; RTXTOXINA.
CC DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4. Repeat; Calcium;
CC Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; Palmitate.
CC KW Transmembrane; 154 170
CC FT TRANSMEM 312 333 POTENTIAL.
CC FT TRANSMEM 393 414 POTENTIAL.
CC FT DOMAIN 625 780 7 x REPEATS, GLY-RICH.
CC FT REPEAT 625 630 1.
CC FT REPEAT 730 735 2.
CC FT REPEAT 739 744 3.
CC FT REPEAT 748 753 4.
CC FT REPEAT 757 762 5.
CC FT REPEAT 766 771 6.
CC FT REPEAT 775 780 7.
CC SQ SEQUENCE 947 AA; 101559 MW; 9744F06395E5BED CRC64;

Query Match 68.4%; Score 39; DB 1; Length 947;
Best Local Similarity 72.7%; Pred. No. 44;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 LSELNKELEAE 12
DB 448 LQNLNKELEAE 458

RESULT 15
YE18_METJA STANDARD; PRT; 181 AA.
ID YE18_METJA
AC 058613;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical aldolase class II protein MJ1418.
GN MJ1418.
OS Methanococcus jannaschii.
OC Archaea: Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN 11)
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

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RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uttenback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Kienk H.-P., Fraser C.M., Smith H.O., Woose C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/EUCA
CC SUBFAMILY. STRONG, TO E.COLI YGBL AND H.INFLUENZAE HI1012.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL: U67582; AAB99428.1; -.
CC DR HSSP: P11550; 3FUA.
CC DR TIGR: MJ1418; -.
CC DR InterPro: IPR001303; Aldolase_II.
CC DR Pfam: PF00596; Aldolase_II; 1.
CC KW Hypothetical protein; Zinc; Complete proteome.
CC FT METAL 68 68 ZINC (BY SIMILARITY).
CC FT METAL 87 87 ZINC (BY SIMILARITY).
CC FT METAL 89 89 ZINC (BY SIMILARITY).
CC FT METAL 147 147 ZINC (BY SIMILARITY).
CC SQ SEQUENCE 181 AA; 20470 MW; E5F3BF1372145B0 CRC64;

```

```

Query Match 66.7%; Score 38; DB 1; Length 181;
Best Local Similarity 70.08%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 FLSELNKELE 10
DB 95 FLSTLNKEIE 104

```

Search completed: September 11, 2002, 09:01:55
Job time: 278 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 09:00:12 : Search time 40.83 Seconds

(Without alignments)
28.241 Million cell updates/sec

Title: US-09-884-696-6

Perfect score: 57

Sequence: 1 FLSELNKLEAE 12

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-71:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	75.4	953	1 B30169	leukotoxin A - Pas
2	43	75.4	955	1 A35254	leukotoxin A - pas
3	43	75.4	956	1 B33389	leukotoxin A - pas
4	43	75.4	956	1 A43834	tox II - Actinob
5	42	73.7	913	2 T52485	neurofilament prot
6	41	71.9	784	2 PN0009	neurofilament trip
7	39	68.4	338	1 B42365	flagellar motor sw
8	39	68.4	332	1 QFPCM	neurofilament trip
9	39	68.4	798	2 T50479	neurofilament medi
10	39	68.4	845	2 A45669	neurofilament trip
11	39	68.4	849	2 S00030	neurofilament trip
12	39	68.4	858	2 S15762	neurofilament trip
13	39	68.4	916	2 A27864	neurofilament trip
14	38	66.7	181	1 A64477	L-fucose-phospha
15	38	66.7	211	2 T03355	gene e12 protein -
16	38	66.7	382	2 E64686	myosin-like protei
17	38	66.7	508	2 T24622	hypothetical prote
18	38	66.7	993	2 C55226	cylm protein - Ent
19	37	64.9	275	2 S21348	probable pol polyp
20	37	64.9	356	2 C40656	regulatory protein
21	37	64.9	359	2 AC1022	two-component sens
22	37	64.9	363	2 F91265	sensor protein Bas
23	37	64.9	363	2 JX0285	sensor protein Bas
24	37	64.9	363	2 C86106	sensor protein for
25	37	64.9	663	2 S69526	hypothetical prote
26	37	64.9	899	2 D96594	unknown protein, 7
27	37	64.9	1534	2 A56734	ribosome receptor,
28	36.5	64.0	617	2 B70425	hypothetical prote
29	36	63.2	117	2 T14283	embryogenic callus

30	36	63.2	159	2 F96794	probable calmodul1
31	36	63.2	196	2 AH1149	hypothetical prote
32	36	63.2	196	2 A11508	hypothetical prote
33	36	63.2	203	2 H83806	hypothetical prote
34	36	63.2	235	2 AF2157	transcription regu
35	36	63.2	379	1 DMDXBF	2-hydroxyglutaryl-
36	36	63.2	462	2 S52528	UAI protein - yea
37	36	63.2	557	2 T47128	heat shock protein
38	36	63.2	828	2 S56250	probable membrane
39	36	63.2	913	2 T25965	hypothetical prote
40	36	63.2	955	2 T21612	hypothetical prote
41	36	63.2	1792	2 T13939	myosin V - fruit f
42	35	61.4	136	2 F97759	hypothetical prote
43	35	61.4	143	2 H71970	hypothetical prote
44	35	61.4	150	2 S60838	M protein precurs
45	35	61.4	152	2 T02703	hypothetical prote

ALIGNMENTS

RESULT 1
B30169
Leukotoxin A - Pasteurella haemolytica (serotype 1)
N:Alternate names: Ikta protein
C:Species: Pasteurella haemolytica
C>Date: 12-Oct-1989 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C:Accession: B30169; C32051; S29516
R:Highlander, S.R.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.
DNA 8, 15-28, 1989
A:Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.
A:Reference number: A30169; MUID:89210283
A:Accession: B30169
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-953 <HIG>
R:Strathdee, C.A.; Lo, R.Y.C.
J. Bacteriol. 171, 916-928, 1989
A:Title: Cloning, nucleotide sequence, and characterization of genes encoding the se
A:Reference number: A32051; MUID:89123172
A:Accession: C32051
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 947-953 <STR>
R:Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E.
Infect. Immun. 55, 1987-1996, 1987
A:Title: Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica A1.
A:Reference number: S29515; MUID:87306837
A:Accession: S29516
A:Molecule type: DNA
A:Residues: 1-741, 'D', 743-953 <LOR>
A:Cross-references: EMBL:M20730; NID:9150492; PIDN:AAA25529.1; PID:9150494
C:Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
C:Genetics:
A:Gene: Ikta
A:Function:
A:Description: lyses leukocytes
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytotoxins; exotoxin; hemolysis; lipoprotein; tandem rep
F:238-784/Domain: hemolysin A homology <HLVA>
F:716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYF]-X)
F:554/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 75.4%; Score 43; DB 1; Length 953;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKLEAE 12
DB 451 FLNLNKLKLEAE 462

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RESULT 2
A:35254
N:Leukotoxin A - Pasteurella haemolytica (serotype T10)
C:Species: Pasteurella haemolytica
C:Date: 10-Aug-1990 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
A:Accession: S37145; A35254; S34237; S34235
R:Latson, A.F.; Alchison, K.; Donachie, W.
Submitted to the EMBL Data Library, September 1993
A:Description: DNA sequence of the leukotoxin A gene from P. haemolytica T10 serotype.
A:Reference number: S37145
A:Accession: S37145
A:Molecule type: DNA
A:Residues: 1-955 <LA1>
A:Cross-references: EMBL:Z26247; NID:9400424; PIDN:CAA81206.1; PID:9400425
J:Highlander, S.K.; Engler, M.J.; Weinstock, G.M.
J: Bacteriol. 172, 2343-2350, 1990
A:Title: Secretion and expression of the Pasteurella haemolytica leukotoxin.
A:Reference number: A35254; MUID:90236888
A:Accession: A35254
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 950-955 <HIC>
A:Cross-references: GB:M24197; GB:M34943; GB:M34944
R:Latson, A.F.; Alchison, K.D.; Donachie, W.
Submitted to the EMBL Data Library, June 1993
A:Description: DNA sequence of the carboxy terminal end of leukotoxin A from the T3 sero
A:Reference number: S34235
A:Accession: S34237
A:Molecule type: DNA
A:Residues: 745-955 <LA2>
A:Cross-references: EMBL:Z22884; NID:9311828; PIDN:CAA80498.1; PID:9311829
A:Experimental source: serotype T3
A:Accession: S34235
A:Molecule type: DNA
A:Residues: 723-955 <LA3>
A:Cross-references: EMBL:Z22887; NID:9311824; PIDN:CAA80501.1; PID:9311825
A:Experimental source: serotype T10
C:Function:
A:Description: attacks cell membranes and causes cell lysis
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
F:240-786/Domain: hemolysin A homology <HLA>
F:718-809/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYF]-X)
F:718-726/Region: repeat
F:727-735/Region: repeat
F:736-744/Region: repeat
F:745-753/Region: repeat
F:754-762/Region: repeat
F:763-771/Region: repeat
F:772-780/Region: repeat
F:781-789/Region: repeat
F:792-800/Region: repeat
F:801-809/Region: repeat
F:556/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 75.4%; Score 43; DB 1; Length 955;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSLNKLEAE 12
II |||||:||
Db 453 FLINLNKLEAE 464

RESULT 3
B33389
N:Alternat names: Actinobacillus pleuropneumoniae
toxin II - Actinobacillus pleuropneumoniae
C:Species: Actinobacillus pleuropneumoniae
C:Date: 09-Mar-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
C:Accession: B33389; S18853; B43599

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R:Chang, Y.F.; Young, R.; Struck, D.K.
DNA 8, 635-647, 1989
A:Title: Cloning and characterization of a hemolysin gene from Actinobacillus (Haemop
A:Reference number: A33389; MUID:90126233
A:Accession: B33389
A:Molecule type: DNA
A:Residues: 1-956 <CHA>
A:Cross-references: GB:M30602; NID:9414823; PIDN:AAA87232.1; PID:9414825
A:Experimental source: serotype 5
R:Smith, M.A.; Braire, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, A.L.J.
Submitted to the EMBL Data Library, July 1991
A:Description: Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
A:Reference number: S18852
A:Accession: S18853
A:Molecule type: DNA
A:Residues: 1-956 <SM1>
A:Cross-references: EMBL:X61111; NID:938939; PIDN:CAA43423.1; PID:938941
R:Smith, M.A.; Braire, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, A.L.J.
Infect. Immun. 59, 4497-4504, 1991
A:Title: Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
A:Reference number: A43599; MUID:92040145
A:Accession: B43599
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27; 948-956 <SM2>
A:Cross-references: GB:X61111; NID:938939
C:Comment: This organism causes porcine pleuropneumonia.
C:Genetics:
A:Gene: apxIIA; appA; clyIIA
C:Function:
A:Description: attacks blood cell membranes and causes cell lysis
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repe
F:243-787/Domain: hemolysin A homology <HLA>
F:719-801/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYF]-X)
F:557/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 75.4%; Score 43; DB 1; Length 956;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSLNKLEAE 12
II |||||:||
Db 455 FLINLNKLEAE 466

RESULT 4
A43834
N:Alternat names: asna protein; cytolysin II; RTX-toxin II
C:Species: Actinobacillus suis
C:Date: 31-Dec-1993 #sequence_revision 08-Nov-1996 #text_change 05-Dec-1998
C:Accession: A43834
R:Burrows, L.L.; Lo, R.Y.
Infect. Immun. 60, 2166-2173, 1992
A:Title: Molecular characterization of an RTX toxin determinant from Actinobacillus s
A:Reference number: A43834; MUID:92267623
A:Accession: A43834
A:Molecule type: DNA
A:Residues: 1-956 <BUR>
A:Experimental source: isolate 3714
A:Note: sequence extracted from NCBI backbone (NCBI:104212, NCBI:104211)
C:Comment: This organism causes acute fatal septicemia in young pigs.
C:Function:
A:Description: attacks cell membranes and causes cell lysis
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repe
F:243-787/Domain: hemolysin A homology <HLA>
F:719-801/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYF]-X)
F:557/Binding site: palmitate (lys) (covalent) #status predicted

```

Query Match 75.4%; Score 43; DB 1; Length 956;
 Best Local Similarity 75.0%; Pred. No. 25;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
 || |||||:||
 DB 455 FLINLNKELOAE 466

RESULT 5
 T52485
 neurofilament protein NF-M(2), middle molecular weight [imported] - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
 C:Accession: T52485
 R:Gervasi, C.; Szaro, B.G.
 Brain Res. Mol. Brain Res. 48, 229-242, 1997
 A:Title: Sequence and expression pattern of two forms of the middle molecular weight neu
 A:Reference number: 226090
 A:Accession: T52485
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-913 <GER>
 A:Cross-references: EMBL:U85970; PIDN:AAB53390.1

Query Match 73.7%; Score 42; DB 2; Length 913;
 Best Local Similarity 66.7%; Pred. No. 35;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
 || : |||||
 DB 106 FLEQNKKELEAE 117

RESULT 6
 PND009
 neurofilament triplet M protein - Pacific electric ray (fragment)
 C:Species: Torpedo californica (Pacific electric ray)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 27-Oct-1995
 C:Accession: PND009
 R:Linal, M.; Scheller, R.H.
 J. Neurochem. 54, 762-770, 1990
 A:Title: A unique neurofilament from Torpedo electric lobe: sequence, expression, and id
 A:Reference number: PND009; MUID:90155300
 A:Accession: PND009
 A:Molecule type: mRNA
 A:Residues: 1-784 <LIN>
 C:Comment: Neurofilaments are a subgroup of intermediate filaments which are expressed s
 C:Superfamily: cytoskeletal keratin
 C:Keywords: coiled coil; cytoskeleton; intermediate filament; nerve; phosphoprotein; tan
 F:1-52/Region: serine-rich
 F:53-84/Region: coil 1a
 F:98-194/Region: coil 1b
 F:217-367/Region: coil 1i
 F:400-597/Region: glutamic acid-rich
 F:598-674/Region: 6 residue repeats
 F:775-784/Domain: carboxyl-terminal #status predicted <CTD>
 F:616,622,628,634,640,646,652,658,670/Binding site: phosphate (Ser) (covalent) #status p

Query Match 71.9%; Score 41; DB 2; Length 784;
 Best Local Similarity 66.7%; Pred. No. 45;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
 :| : |||||
 DB 72 YLEQNKKELEAE 83

RESULT 7
 B42365
 flagellar motor switch protein flig - Bacillus subtilis

C:Species: Bacillus subtilis
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: B42365; C69624; S14495
 R:Albertini, A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Gallizzi, A.
 J. Bacteriol. 173, 3573-3579, 1991
 A:Title: The flia locus of Bacillus subtilis is part of a large operon coding for fl
 A:Reference number: A42365; MUID:91258343
 A:Accession: B42365

A:Molecule type: DNA
 A:Residues: 1-338 <ALB>
 A:Cross-references: EMBL:X56049; NID:g39904; PIDN:CA39521.1; PID:g39905
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be
 C.; Bron, S.; Bruggli, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 A.; Ehrlich, S.D.; Emerson, P.T.; Eutlian, K.D.; Erington, J.; Fabret, C.; Ferrari,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Ga
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, I
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardic
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mei
 Y., M.; Ogawa, K.; Ogilwa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scan
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; S
 akuchl, M.; Yamakoshi, A.; Tanaka, T.; Tepstra, P.; Tognoni, A.; Tosato, V.; Uchiy
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshid
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
 A:Reference number: A69580; MUID:98044033

A:Accession: C69624
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-338 <RUN>
 A:Cross-references: GB:299112; GB:AL009126; NID:g2633902; PIDN:CA313495.1; PID:g2633
 A:Experimental source: strain 168

A:Gene: flig
 C:Superfamily: flagellar rotation
 C:Keywords: flagellar rotation

Query Match 68.4%; Score 39; DB 1; Length 338;
 Best Local Similarity 72.7%; Pred. No. 41;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LSELNKELEAE 12
 ||||| :|||
 DB 150 LSELNPEVOAE 160

RESULT 8
 QPFCM
 neurofilament triplet M protein - pig (fragments)
 N:Alternate names: 160K neurofilament protein; NF-M(medium) protein; type IV IF prot
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 31-Mar-1988 #sequence_revision 02-Jul-1998 #text_change 10-Jul-1998
 C:Accession: A05075; S02570
 R:Geisler, N.; Fischer, S.; Vandekerckhove, J.; Plessmann, U.; Weber, K.
 EMBO J. 3, 2701-2706, 1984
 A:Title: Hybrid character of a large neurofilament protein (NF-M): intermediate filam
 A:Reference number: A05075; MUID:85076594

A:Accession: A05075
 A:Molecule type: protein
 A:Residues: 1-454 <GEI>
 A:Experimental source: spinal cord
 R:Geisler, N.; Vandekerckhove, J.; Weber, K.
 FEBS Lett. 221, 403-407, 1987
 A:Title: Location and sequence characterization of the major phosphorylation sites o
 A:Reference number: S02570; MUID:87304852

A:Accession: S02570
 A:Molecule type: protein
 A:Residues: 438-450; 455-459; 460-475; 476-514; 515-532 <GEI2>
 A:Experimental source: spinal cord
 C:Superfamily: cytoskeletal keratin
 C:Keywords: blocked amino end; coiled coil; intermediate filament; phosphoprotein

F:1-98/Domain: head #status predicted <HED>
F:99-412/Domain: alpha-helical rod <ROD>
F:438-454,465-459,476-514/Domain: tail (fragments) #status predicted <TRIP1>
F:515-532/Domain: tail (fragment) #status predicted <TRIP2>
F:1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental
F:456,462,465,479/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 68.4%; Score 39; DB 1; Length 532;
Best Local Similarity 58.3%; Pred. No. 66;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSLNKLEAE 12
: | : |||: |||
Db 121 YLEQNKLEAE 132

RESULT 9
150479
neurofilament medium protein - goldfish
C:Species: Carassius auratus (goldfish)
C>Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text_change 13-Aug-1999
C:Accession: 150479
R:Glasgow, E.; Hall, C.M.; Schechter, N.
J. Neurochem. 63, 52-61, 1994
A:Title: Organization, sequence, and expression of a gene encoding goldfish neurofilament
A:Reference number: 150479; MUID:94267484
A:Accession: 150479
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-798 <GLA>
A:Cross-references: GB:L09742; NID:g213019; PIDN:AAA72341.1; PID:g213020
C:Genetics:
A:introns: 343/3; 385/2
A:introns: 343/3; 385/2
C:Superfamily: cytoskeletal keratin

Query Match 68.4%; Score 39; DB 2; Length 798;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSLNKLEAE 12
: | : |||: |||
Db 104 FLEQNKLEAE 115

RESULT 10
A45669
neurofilament triplet M protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 13-Aug-1999
C:Accession: A45669; S25712; A42393
R:Napolitano, E.W.; Chin, S.S.M.; Colman, D.R.; Liem, R.K.H.
J. Neurosci. 7, 2590-2599, 1987
A:Title: Complete amino acid sequence and in vitro expression of rat NF-M, the middle mo
A:Reference number: A45669; MUID:87282618
A:Accession: A45669
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-845 <NAP>
A:Cross-references: EMBL:M18628; NID:g205687; PIDN:AAA41696.1; PID:g205688
R:Kelly, B.M.; Gillespie, C.S.; Sherman, D.L.; Brophy, P.J.
J. Cell Biol. 118, 397-410, 1992
A:Title: Schwann cells of the myelin-forming phenotype express neurofilament protein NF-
A:Reference number: S25712; MUID:92332556
A:Accession: S25712
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17,19-21,'P',23-204,'L',206-500,'E',501-845 <REL>
A:Cross-references: EMBL:212152; NID:g56751; PIDN:CAA78136.1; PID:g56752
R:Xu, Z.S.; Liu W.S.; Willard, M.B.
J. Biol. Chem. 267, 4467-4471, 1992
A:Title: Identification of six phosphorylation sites in the COOH-terminal tail region of

A:Reference number: A42393; MUID:92165797
A:Accession: A42393
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 411-500,'E',501-843,'D' <XID>
A:Note: sequence extracted from NCBI backbone (NCBIP:83873)
C:Superfamily: cytoskeletal keratin

Query Match 68.4%; Score 39; DB 2; Length 845;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSLNKLEAE 12
: | : |||: |||
Db 120 YLEQNKLEAE 131

RESULT 11
S00030
neurofilament triplet M protein - mouse
N:Alternate names: 160K NF protein; NF-M
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: S00030
R:Levy, E.; Liem, R.K.H.; d'Eustachio, P.; Cowan, N.J.
Eur. J. Biochem. 166, 71-77, 1987
A:Title: Structure and evolutionary origin of the gene encoding mouse NF-M, the middl
A:Reference number: S00030; MUID:87246594
A:Accession: S00030
A:Molecule type: DNA
A:Residues: 1-849 <LEV>
A:Cross-references: GB:X05640; NID:g53357; PIDN:CAA29127.1; PID:g297529
C:Genetics:
A:Map position: 14
A:introns: 359/3; 401/2
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:99-244/Domain: coiled coil <COL>
F:267-411/Domain: coiled coil <CO2>
F:412-849/Domain: tail <TAI>

Query Match 68.4%; Score 39; DB 2; Length 849;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSLNKLEAE 12
: | : |||: |||
Db 120 YLEQNKLEAE 131

RESULT 12
S15762
neurofilament triplet M protein - chicken
C:Species: Gallus gallus (chicken)
C>Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 13-Aug-1999
C:Accession: S15762; S08061; A27040
R:Zopf, D.; Dineva, B.; Betz, H.; Gundelfinger, E.D.
Nucleic Acids Res. 18, 521-529, 1990
A:Title: Isolation of the chicken middle-molecular weight neurofilament (NF-M) gene a
A:Reference number: S15762; MUID:90174973
A:Accession: S15762
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-858 <ZOP>
A:Cross-references: EMBL:X17102; NID:g63688; PIDN:CAA34958.1; PID:g63689
R:Zopf, D.; Dineva, B.; Betz, H.; Gundelfinger, E.
submitted to the EMBL Data Library, November 1989
A:Reference number: S08061
A:Accession: S08061
A:Molecule type: DNA
A:Residues: 1-355,368-858 <Z02>

A:Cross-references: EMBL:X17102
R:20p1, D.; Hermans-Borgmeyer, I.; Gundelfinger, E.D.; Betz, H.
Genes Dev. 1, 699-708, 1987
A:Title: Identification of gene products expressed in the developing chick visual system
A:Reference number: A27040; MUID:88112814
A:Accession: A27040
A:Molecule type: mRNA
A:Residues: 350-546; /R/548-858 <Z03>
A:Cross-references: GB:X05558; NID:g63685; PIDN:CAA29073.1; PID:g63686
C:Genetics:
A:Introns: 355/3; 397/2
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

Query Match 68.4%; Score 39; DB 2; Length 858;
Best Local Similarity 58.3%; Pred. No. 1;Le+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
| : |||:|

Db 116 YLEQNKKEIRAE 127

RESULT 13
A27864
neurofilament triplet M protein - human
N:Alternate names: NF-M (medium) protein
C:Species: Homo sapiens (hmn)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: A27864; A30157
R:Myers, M.W.; Lazzarini, R.A.; Lee, V.M.Y.; Schlaepfer, W.W.; Nelson, D.L.
EMBO J. 6, 1617-1626, 1987
A:Title: The human mid-size neurofilament subunit: a repeated protein sequence and the
A:Reference number: A27864; MUID:87275853
A:Accession: A27864
A:Molecule type: DNA
A:Residues: 1-916 <MYE>
A:Cross-references: GB:Y00067; NID:g35045; PIDN:CAA68276.1; PID:g35046
R:Lee, V.M.Y.; Olivos Jr., L.; Carden, M.J.; Hollosi, M.; Dietzschold, B.; Lazzarini, R.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 1998-2002, 1988
A:Title: Identification of the major multiphosphorylation site in mammalian neurofilament
A:Reference number: A30157; MUID:88158120
A:Contents: annotation; phosphorylation sites
C:Genetics:
A:Introns: 360/3; 402/2
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; phosphoprotein
F:615,628,641,654,680/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 68.4%; Score 39; DB 2; Length 916;
Best Local Similarity 58.3%; Pred. No. 1;2e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
| : |||:|

Db 121 YLEQNKKEIRAE 132

RESULT 14
A64477
L-fucose-phosphate aldolase homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C:Accession: A64477
R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weissflog, K.G.; Merrick, J.M.; Glodex, A.;
rson, J.D.; Sedov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999

A:Accession: A64477
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-181 <BU>
A:Cross-references: GB:067582; GB:L77117; NID:g1592064; PIDN:AA899428.1; PID:g159206
C:Genetics:
A:Map position: FOR138152-1381697
C:Superfamily: L-ribulose-phosphate 4-epimerase

Query Match 66.7%; Score 38; DB 1; Length 181;
Best Local Similarity 70.0%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 10
|| : |||:|

Db 95 FLSELNKELEAE 104

RESULT 15
T03355
gene e12 protein - Lactococcus phage bL170
C:Species: Lactococcus phage bL170
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 04-Mar-2000
C:Accession: T03355
R:Crutz-Le Cog, A.M.; Cesselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopi
submitted to the EMBL Data Library, June 1997
A:Description: Sequence and organization of the lactococcal isometric bL170 phage g
A:Reference number: Z14903
A:Accession: T03355
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-211 <CRU>
A:Cross-references: EMBL:AF009630; NID:g3282260; PIDN:AA027226.1; PID:g3282307
C:Genetics:
A:Gene: e12
C:Superfamily: Lactococcus phage bL170 gene e12 protein

Query Match 66.7%; Score 38; DB 2; Length 211;
Best Local Similarity 81.8%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 LSELNKELEAE 12
||| |||||

Db 151 LSEQNKKEIRAE 161

Search completed: September 11, 2002, 09:00:14
Job time: 232 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:59:25 : Search time 30.68 Seconds
(without alignments)
9.554 Million cell updates/sec

Title: US-09-884-696-6

Sequence: 1 FLSELNKLEAE 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	75.4	924	3	US-08-619-812-8
2	43	75.4	926	1	US-07-908-253-2
3	43	75.4	926	1	US-08-455-970A-2
4	43	75.4	926	1	US-08-387-156-6
5	43	75.4	926	2	US-08-694-865-6
6	43	75.4	926	2	US-08-878-748-6
7	43	75.4	926	2	US-08-535-837-2
8	43	75.4	926	3	US-09-124-491-6
9	43	75.4	926	6	5476557-3
10	43	75.4	936	1	US-08-455-970A-12
11	43	75.4	943	1	US-08-455-970A-10
12	43	75.4	951	1	US-08-455-970A-14
13	43	75.4	956	3	US-08-772-770A-8
14	43	75.4	977	1	US-08-387-156-8
15	43	75.4	977	2	US-08-694-865-8
16	43	75.4	977	2	US-08-878-748-8
17	43	75.4	977	3	US-09-124-491-8
18	43	75.4	1069	1	US-07-777-715-9
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20	43	75.4	1069	3	US-08-954-418-4
21	43	75.4	1098	1	US-07-777-715-7
22	43	75.4	1098	1	US-08-170-126-2
23	43	75.4	1098	3	US-08-954-418-2
24	39	68.4	934	1	US-08-215-805A-80
25	37	64.9	30	4	US-09-623-618B-21
26	37	64.9	31	4	US-09-623-618B-20
27	37	64.9	2763	3	US-08-496-944-2

28	35	61.4	229	4	US-09-045-973-7	Sequence 7, Appl
29	35	61.4	1866	4	US-08-938-105-3	Sequence 3, Appl
30	35	61.4	1939	4	US-09-310-187A-1	Sequence 1, Appl
31	34	59.6	20	1	US-08-468-543-10	Sequence 10, Appl
32	34	59.6	20	2	US-08-469-692-10	Sequence 10, Appl
33	34	59.6	20	2	US-08-398-046-10	Sequence 10, Appl
34	34	59.6	22	1	US-07-928-930A-8	Sequence 8, Appl
35	34	59.6	22	1	US-08-288-568-8	Sequence 8, Appl
36	34	59.6	22	1	US-08-487-461-8	Sequence 8, Appl
37	34	59.6	22	1	US-08-432-691-8	Sequence 8, Appl
38	34	59.6	22	1	US-08-487-459-8	Sequence 8, Appl
39	34	59.6	22	3	US-08-940-095-75	Sequence 75, Appl
40	34	59.6	22	3	US-08-940-095-106	Sequence 106, Appl
41	34	59.6	22	3	US-08-940-095-119	Sequence 119, Appl
42	34	59.6	22	3	US-08-940-095-121	Sequence 121, Appl
43	34	59.6	22	3	US-08-940-093-75	Sequence 75, Appl
44	34	59.6	22	3	US-08-940-093-106	Sequence 106, Appl
45	34	59.6	22	3	US-08-940-093-119	Sequence 119, Appl

ALIGNMENTS

RESULT 1

US-08-619-812-8

Sequence 8, Application US/08619812

Patent No. 6100066

GENERAL INFORMATION:

APPLICANT: POTTER, ANDREW A.

APPLICANT: THEISEN, MICHAEL

APPLICANT: HARLAND, RICHARD J.

APPLICANT: RIOUX, CLEMENT R.

TITLE OF INVENTION: VACCINES FOR HAEMOPHILUS SOMNUS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS

STREET: 635 BRYANT STREET

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/619,812

FILING DATE: 15-MAR-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/038,719

FILING DATE: 29-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 924 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-619-812-8

Query Match: 75.4% Score 43; DB 3; Length 924;
Best Local Similarity 75.0% Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSEINKELAE 12
11 11111111
DB 424 FLINLNKELQAE 435

RESULT 2

US-07-908-253-2
Sequence 2, Application US/07908253
Patent No. 5534256
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,253
FILING DATE: 19920702
CLASSIFICATION: 420
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-908-253-2

Query Match 75.4%; Score 43; DB 1; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSEINKELAE 12
11 11111111
DB 424 FLINLNKELQAE 435

RESULT 3

US-08-455-970A-2
Sequence 2, Application US/08455970A
Patent No. 5708155
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HOW P. A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
TITLE OF INVENTION: CHIMERAS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,970A

FILING DATE: 31-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/960,932

FILING DATE: 14-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016.10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 327-3400

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 926 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-455-970A-2

QY 1 FLSEINKELAE 12
11 11111111
DB 424 FLINLNKELQAE 435

RESULT 4

US-08-387-156-6
Sequence 6, Application US/08387156
Patent No. 5723129
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HOW P. A.
TITLE OF INVENTION: GHRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-387-156-6

Query Match 75.4%; Score 43; DB 1; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
|| |||||:
Db 424 FLNLNKELOAE 435

RESULT 5
US-08-694-865-6
Sequence 6, Application US/08694865
Patent No. 5837268
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNIS, JOHN G.
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,865
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-694-865-6

Query Match 75.4%; Score 43; DB 2; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
|| |||||:
Db 424 FLNLNKELOAE 435

RESULT 6

US-08-878-748-6
Sequence 6, Application US/08878748
Patent No. 5969126
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUI P. A.
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,748
FILING DATE: 19-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-878-748-6

Query Match 75.4%; Score 43; DB 2; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
|| |||||:
Db 424 FLNLNKELOAE 435

RESULT 7
US-08-535-837-2
Sequence 2, Application US/08535837
Patent No. 5985289
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: HEMOPHILUS SOMNUS OUTER MEMBRANE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA

Query Match 75.4%; Score 43; DB 2; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,837
FILING DATE: 27-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0026.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-535-837-2

Query Match 75.4%; Score 43; DB 2; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
|| |||||:
Db 424 FLNLNKELEAE 435

RESULT 8
US-09-124-491-6
Sequence 6, Application US/09124491
Patent No. 6022960
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANN, JOHN G.
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,491
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:

NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-491-6

Query Match 75.4%; Score 43; DB 3; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
|| |||||:
Db 424 FLNLNKELEAE 435

RESULT 9
5476657-3
Patent No. 5476657
APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA LEUKOTOXIN
COMPOSITIONS AND USES THEREOF
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/15,537
FILING DATE: 09-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,850
FILING DATE: 05-APR-1990
APPLICATION NUMBER: 335,018
FILING DATE: 07-APR-1989
SEQ ID NO:3:
LENGTH: 926
5476657-3

Query Match 75.4%; Score 43; DB 6; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
|| |||||:
Db 424 FLNLNKELEAE 435

RESULT 10
US-08-455-970A-12
Sequence 12, Application US/08455970A
Patent No. 5708155
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,970A
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0016.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
;
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 936 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-455-970A-12

Query Match          75.4%; Score 43; DB 1; Length 936;
Best Local Similarly 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
Db 424 FLNLNKELEQAE 435

RESULT 11
US-08-455-970A-10
; Sequence 10, Application US/08455970A
; Patent No. 5708155
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HUM P.A.
; TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,970A
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0016.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
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; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-455-970A-14

Query Match          75.4%; Score 43; DB 1; Length 943;
Best Local Similarly 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
Db 424 FLNLNKELEQAE 435

RESULT 12
US-08-455-970A-14
; Sequence 14, Application US/08455970A
; Patent No. 5708155
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HUM P.A.
; TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0016.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
;
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 951 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-455-970A-14
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-455-970A-10

Query Match          75.4%; Score 43; DB 1; Length 943;
Best Local Similarly 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
Db 424 FLNLNKELEQAE 435

RESULT 12
US-08-455-970A-14
; Sequence 14, Application US/08455970A
; Patent No. 5708155
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HUM P.A.
; TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,970A
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0016.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
;
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 951 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-455-970A-14

Query Match          75.4%; Score 43; DB 1; Length 951;
Best Local Similarly 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
Db 424 FLNLNKELEQAE 435

RESULT 13
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US-08-772-270A-8
; Sequence 8, Application US/08772270A
; Patent No. 6019984
; GENERAL INFORMATION:
; APPLICANT: MacInnes, Janet
; APPLICANT: Ricciatti, Paul
; APPLICANT: Mallard, Bonnie
; APPLICANT: Rosendal, Soren
; TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR
; TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bereskin & Parr
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,270A
; FILING DATE: December 23, 1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 6580-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 956 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Actinobacillus pleuropneumoniae
; US-08-772-270A-8

Query Match 75.4%; Score 43; DB 3; Length 956;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
|| |||||:
Db 455 FLINLNKELOAE 466

RESULT 14
US-08-387-156-8
; Sequence 8, Application US/08387156
; Patent No. 5723129
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HOW P.A.
; TITLE OF INVENTION: GnRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,156
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,171
; FILING DATE: 16-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0016.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-387-156-8

Query Match 75.4%; Score 43; DB 1; Length 977;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
|| |||||:
Db 424 FLINLNKELOAE 435

RESULT 15
US-08-694-865-8
; Sequence 8, Application US/08694865
; Patent No. 5837268
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: MANN, JOHN G.
; TITLE OF INVENTION: GnRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS LLP
; STREET: 265 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/694,865
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 9001-0016.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)327-3231
; TELEFAX: (415)327-3231
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 977 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-694-865-8

Query Match 75.4%; Score 43; DB 2; Length 977;
 Best Local Similarity 75.0%; Pred. NO. 16;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FISELNKELEAE 12
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 DB 424 FLINKNKELEAE 435

Search completed: September 11, 2002, 08:59:26
 Job time: 209 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2002, 09:01:26 : Search time 65.81 Seconds
(without alignments)
36.802 Million cell updates/sec

Title: US-09-884-696-13

Perfect score: 77

Sequence: 1 FNDIFHSGEGDDL 14

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 10%

Listing first 45 summaries

Database :

SPREMBL_19:*

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- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.rodent:*
- 12: sp.virus:*
- 13: sp.vertebrate:*
- 14: sp.unclassified:*
- 15: sp.virus:*
- 16: sp.bacteriopl:*
- 17: sp.archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	927	2	093G12 moraxella b
2	59	76.6	1055	2	043892 actinobacil
3	58	75.3	1049	2	09RCG8 pasteurella
4	58	75.3	1052	2	093NP0 actinobacil
5	52	67.5	998	2	046716 escherichia
6	52	67.5	998	2	09LC58 escherichia
7	52	67.5	998	2	085101 escherichia
8	52	67.5	998	2	047262 escherichia
9	52	67.5	998	2	047461 escherichia
10	52	67.5	998	2	047461 escherichia
11	50	64.9	387	16	092UA7 rhizobium m
12	49	63.6	208	2	051868 pasteurella
13	49	63.6	233	2	051865 pasteurella
14	49	63.6	946	2	09EV24 manheimia
15	49	63.6	953	2	09ETX2 manheimia
16	49	63.6	953	2	09ETG5 pasteurella

17	49	63.6	953	2	09EV34 pasteurella
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28	49	63.6	955	2	09EV22 pasteurella
29	49	63.6	1022	2	093NP2 actinobacil
30	48	62.3	334	17	029369 archaeoglob
31	48	62.3	953	2	09EV30 pasteurella
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33	46	59.7	644	16	092UD8 rhizobium m
34	46	59.7	956	2	093NP1 actinobacil
35	46	59.7	958	2	033527 rhizobium l
36	45	58.4	567	2	09RH2 pseudomonas
37	45	58.4	1771	16	P74647 synchocyst
38	44	57.1	856	2	09ZFG9 azotobacter
39	43	55.8	219	16	P96437 rhizobium m
40	43	55.8	359	16	092KC8 rhizobium m
41	43	55.8	1112	16	092UV3 rhizobium m
42	43	55.8	1360	12	09IKD1 rat stailoda
43	42.5	54.5	1401	2	085374 proteus mir
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ALIGNMENTS

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DT	01-DEC-2001	(TREMBlrel. 19, Last sequence update)																									
DT	01-DEC-2001	(TREMBlrel. 19, Last annotation update)																									
DE	RTX TOXIN.																										
GN	MBXA.																										
OS	Moraxella bovis.																										
OC	Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.																										
OX	NCBI_TaxID=476;																										
RN	[1]																										
RP	SEQUENCE FROM N.A.																										
RC	STRAIN=TIFTON 1;																										
RA	MEDLINE=21388402; PubMed=11497442;																										
RT	Angelos J.A., Hess J.F., George L.W.;																										
RL	"Cloning and characterization of a Moraxella bovis cytotoxin gene.";																										
DR	Am. J. Vet. Res. 62:1222-1228(2001).																										
SO	EMBL: AF205359; AAK84651.1; "																										
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Query Match																											
Best Local Similarity																											
Matches 14; Conservative																											
0; Mismatches																											
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0; Gaps																											
0;																											
QY	1 FNDIFHSGEGDDL 14																										
Db	705 FNDIFHSGEGDDL 718																										
RESULT	2																										
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DT	01-NOV-1996	(TREMBlrel. 01, Created)																									
DT	01-NOV-1996	(TREMBlrel. 01, Last sequence update)																									
DT	01-DEC-2001	(TREMBlrel. 19, Last annotation update)																									

DE LEUKOTOXIN.
GN I.K.T.A.
OS Actinobacillus actinomycetemcomitans (Haemophilus
OC actinomycetemcomitans).
OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JP2;
RA Kolodrubetz J., Bailey T., Kraig E.;
RT "Nucleotide sequence of the leukotoxin gene from actino-bacillus
KT Actinomycetemcomitans: Homology to the A-hemolysin/leukotoxin gene
RT family";
RL Infect. Immun. 58:920-929(1991).
DR EMBL: X16829; CAA34731.1; -
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003995; RTX_A.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR001441; OIP_synth.
DR Pfam: PF00353; hemolysincabind; 3.
DR Pfam: PF02382; RTX_1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PRINTS: PR01488; RTXTOXIN_A.
DR PROSITE: PS00330; HEMOLYSIN_CALCITUM; 3
SQ SEQUENCE 1055 AA; 113853 MW; 531C396FA76669E CRC64;

Query Match 76.6%; Score 59; DB 2; Length 1055;
Best Local Similarity 64.3%; Pred. No. 0.13;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 FNDIFHSGEGDDL 14
Db 734 FNDVFGHGDGDL 747

RESULT 3
Q9RCG8 PRELIMINARY; PRT; 1049 AA.
AC Q9RCG8;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE PAXA.
GN PAXA.
OS Pasteurella aerogenes.
OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=749;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FIELD STRAIN JF1319;
RA Heyberger-Meyer B., Frey J., Nicolet J., Kuhnert P.;
RT "Identification and characterization of a new RTX toxin operon (pax)
RT in Pasteurella aerogenes";
RL Submitted (MUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U66588; AAF15370.1; -
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003995; RTX_A.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysincabind; 2.
DR Pfam: PF02382; RTX_1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PRINTS: PR01488; RTXTOXIN_A.
DR PROSITE: PS00330; HEMOLYSIN_CALCITUM; 2
SQ SEQUENCE 1049 AA; 112308 MW; 9FA5070EA48C3127 CRC64;

Query Match 75.3%; Score 58; DB 2; Length 1049;
Best Local Similarity 71.4%; Pred. No. 0.19;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNDIFHSGEGDDL 14
Db 748 FRDIFGADGDDL 761

RESULT 4
Q93NPO PRELIMINARY; PRT; 1052 AA.
AC Q93NPO;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE RTX-TOXIN IIA.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OX NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin S.J., Park J.Y., Choi I.S., Shin N.R., Yoo H.S.;
RT "Cloning and Sequencing of Apx IIA from Actinobacillus
RT pleuropneumoniae";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF363363; AAK50053.1; -
SQ SEQUENCE 1052 AA; 112862 MW; CA0E160F02101FA2 CRC64;

Query Match 75.3%; Score 58; DB 2; Length 1052;
Best Local Similarity 71.4%; Pred. No. 0.19;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNDIFHSGEGDDL 14
Db 748 FRDIFGADGDDL 761

RESULT 5
Q46716 PRELIMINARY; PRT; 998 AA.
AC Q46716;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE HEMOLYSIN A (HLXA).
GN HLXA OR EHEC-HLXA.
OS Escherichia coli O157:H7.
OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98290540; Pubmed=9628576;
RA Makino K., Ishii K., Yasunaga T., Hattori M., Yokoyama K.,
RA Matsuda H.C., Kubota Y., Yamachi Y., Iida T., Yamamoto K., Honda T.,
RA Han C., Ohtsubo A., Kasamatsu M., Hayashi T., Kuwara S., Shinagawa H.;
RT "Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an
RT enterohemorrhagic Escherichia coli O157:H7 derived from Sakai
RT outbreak";
RL DNA Res. 5:1-9(1998).
RN [2]
RP SEQUENCE OF 241-998 FROM N.A.
RC STRAIN-EHEC;
RA Hall R.H., Xu J., Walderhaug M.O.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=EDL933;
RX MEDLINE=98391744; Pubmed=9722640;
RA Burland V., Shao Y., Perna N.T., Plunkett G., Sofia H.J.,
RA Blattner F.R.;
RT "The complete DNA sequence and analysis of the large virulence plasmid
RT of Escherichia coli O157:H7";

RL Nucleic Acids Res. 26:4196-4204(1998).
 DR EMBL: AB011549; BAA31774.1; -
 DR EMBL: U12572; AAA20544.1; -
 DR EMBL: AF074613; AAC70116.1; -
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003995; RTX_A.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam: PF00353; hemolysinCabin; 2.
 DR Pfam: PF02382; RTX; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PRINTS: PR01488; RTXTOXINA.
 DR PROSITE: PS00330; HEMOLYSIN_CALCITUM; 2.
 KW Plasmid.
 SQ SEQUENCE 998 AA; 107047 MW; BB3CD36FCBB9EBD CRC64;

Query Match 67.5%; Score 52; DB 2; Length 998;
 Best Local Similarity 57.1%; Pred. No. 2;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNDIFHSGEDDL 14
 ||||| :|:| :
 Db 720 FNDIFHSGDNDYI 733

RESULT 6
 Q9LC58 PRELIMINARY; PRT; 998 AA.

AC Q9LC58;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE HEMOLYSIN A.
 GN EHEC-HLYA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanelike I., Wakisaka-Saito N., Harada Y., Zhang H.-M., Yamamoto T.;
 RT "The enterohemorrhagic Escherichia coli (EHEC)-hemolysin genes of a
 RT Shiga toxin 1 (Stx1)- and Stx2-producing, serotype O128 Escherichia
 RT coli strain with a greatest hemolytic activity.";
 RL Acta Med. Biol. (Mligata) 0:0-0(2000).
 DR EMBL: AB032930; BAA93708.1; -
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam: PF00353; hemolysinCabin; 2.
 DR Pfam: PF02382; RTX; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PROSITE: PS00330; HEMOLYSIN_CALCITUM; 2.
 SQ SEQUENCE 998 AA; 107196 MW; CD7A88E9BD862DB6 CRC64;

Query Match 67.5%; Score 52; DB 2; Length 998;
 Best Local Similarity 57.1%; Pred. No. 2;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNDIFHSGEDDL 14
 ||||| :|:| :
 Db 720 FNDIFHSGDNDYI 733

RESULT 7
 O85101 PRELIMINARY; PRT; 998 AA.

DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HEMOLYSIN.
 GN EHX.

OS Escherichia coli.
 OG Plasmid EHEC-hemolysin plasmid.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ENTEROHEMORRHAGIC EC920006;
 RX MEDLINE=98261495; PubMed=9596716;
 RA Berlin P., Chen S., Colbourne J.K., Johnson R., De Grandis S.,
 RA Gyles C.;
 RT "Evolution of enterohemorrhagic escherichia coli hemolysin plasmids
 RT and the locus for enterocyte effacement in Shiga toxin-producing E.
 RT coli.";
 RL Infect. Immun. 66:2553-2561(1998).
 DR EMBL: AF043471; AAC24352.1; -
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003995; RTX_A.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam: PF00353; hemolysinCabin; 2.
 DR Pfam: PF02382; RTX; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PRINTS: PR01488; RTXTOXINA.
 DR PROSITE: PS00330; HEMOLYSIN_CALCITUM; 2.
 KW Plasmid.
 SQ SEQUENCE 998 AA; 107095 MW; E5A56B239DCBE55 CRC64;

Query Match 67.5%; Score 52; DB 2; Length 998;
 Best Local Similarity 57.1%; Pred. No. 2;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNDIFHSGEDDL 14
 ||||| :|:| :
 Db 720 FNDIFHSGDNDYI 733

RESULT 8
 Q47262 PRELIMINARY; PRT; 998 AA.

AC Q47262;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HEMOLYSIN.
 GN EHEC-HLYA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95172699; PubMed=7868227;
 RA Schmidt H., Beutin L., Karch H.;
 RT "Molecular analysis of the plasmid-encoded hemolysin of Escherichia
 RT coli O157:H7 strain E1933.";
 RL Infect. Immun. 63:1055-1061(1995).
 DR EMBL: X79839; CAA56234.1; -
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003995; RTX_A.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam: PF00353; hemolysinCabin; 2.
 DR Pfam: PF02382; RTX; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PRINTS: PR01488; RTXTOXINA.
 DR PROSITE: PS00330; HEMOLYSIN_CALCITUM; 2.
 SQ SEQUENCE 998 AA; 107058 MW; OD3BE108C309B8B3 CRC64;

Query Match 67.5%; Score 52; DB 2; Length 998;
 Best Local Similarity 57.1%; Pred. No. 2;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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OY      1 FNDIFHSGEGDDL 14
      11111 :1:1 :
Db      720 FNDIFHGADGNDYI 733

RESULT  9
ID      047461      PRELIMINARY;      PRT;      998 AA.
AC      047461;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      EHEC-HLYA PROTEIN.
GN      EHEC-HLYA.
OS      Escherichia coli.
OG      Plasmid p0157.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX      Escherichia.
NCBI_TaxID=562;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-EDL 933;
RX      MEDLINE=95172699; PubMed=7868227;
RA      Schmidt H., Beutin L., Karch H.;
RT      "Molecular analysis of the plasmid-encoded hemolysin of Escherichia
RT      coli 0157:H7 strain Edl933."
RL      Infect. Immun. 63:1055-1061(1995).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN-EDL 933;
RX      MEDLINE=97090409; PubMed=8936317;
RA      Schmidt H., Kernbach C., Karch H.;
RT      "Analysis of the EHEC hly operon and its location in the physical map
RT      of the large plasmid of enterohemorrhagic Escherichia coli 0157:H7."
RL      Microbiology 142:907-914(1996).
DR      EMBL; X86087; CAA60042.1; -
DR      InterPro: IPR001343; HemlYsn_Ca_bind.
DR      InterPro: IPR003995; RTX.N.
DR      InterPro: IPR003355; RTX.N.
DR      Pfam; PF00353; hemolysincbind; 2.
DR      Pfam; PF02382; RTX; 1.
DR      PRINTS; PR00313; CABNDNGRPT.
DR      PRINTS; PR01488; RTXTOXINA.
DR      PROSITE; PS00330; HEMOLYSIN_CALCITUM; 2.
KW      Plasmid
SQ      SEQUENCE 998 AA; 107032 MW; 4D8BE108C309BF7E CRC64;

Query Match      67.5%; Score 52; DB 2; Length 998;
Best Local Similarity 57.1%; Pred. No. 2;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY      1 FNDIFHSGEGDDL 14
      11111 :1:1 :
Db      720 FNDIFHGADGNDYI 733

RESULT 10
ID      P71223      PRELIMINARY;      PRT;      998 AA.
AC      P71223;
DT      01-FEB-1997 (TREMBlrel. 02, Created)
DT      01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      EHEC-HEMOLYSIN.
GN      EHEC-HLYA.
OS      Escherichia coli.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX      Escherichia.
NCBI_TaxID=562;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-78-92;

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RX      MEDLINE=97034824; PubMed=8880480;
RA      Schmidt H., Karch H.;
RT      "Enterohemolytic phenotypes and genotypes of Shiga Toxin-producing
RT      Escherichia coli 0111 strain from patients with diarrhea and hemolytic-
RT      uremic syndrome."
RL      J. Clin. Microbiol. 34:2364-2367(1996).
DR      EMBL; X94129; CAA63849.1; -
DR      InterPro: IPR001343; HemlYsn_Ca_bind.
DR      InterPro: IPR003995; RTX.N.
DR      InterPro: IPR003355; RTX.N.
DR      Pfam; PF00353; hemolysincbind; 2.
DR      Pfam; PF02382; RTX; 1.
DR      PRINTS; PR00313; CABNDNGRPT.
DR      PRINTS; PR01488; RTXTOXINA.
DR      PROSITE; PS00330; HEMOLYSIN_CALCITUM; 2.
SQ      SEQUENCE 998 AA; 107255 MW; DA3EF078C7E4131E CRC64;

Query Match      67.5%; Score 52; DB 2; Length 998;
Best Local Similarity 57.1%; Pred. No. 2;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY      1 FNDIFHSGEGDDL 14
      11111 :1:1 :
Db      720 FNDIFHGADGNDYI 733

RESULT 11
ID      092UA7      PRELIMINARY;      PRT;      387 AA.
AC      092UA7;
DT      01-DEC-2001 (TREMBlrel. 19, Created)
DT      01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      HYPOTHELICAL CALCIUM BINDING PROTEIN SMB21402.
GN      SMB21402.
OS      Rhizobium meliloti (Sinorhizobium meliloti).
OC      Plasmid pSymb (megaplasmid 2).
OC      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC      Rhizobiaceae; Sinorhizobium.
OX      NCBI_TaxID=382;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-1021;
RX      MEDLINE=21396508; PubMed=11481431;
RA      Flinn T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA      Vorhölter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA      Golding B., Puehler A.;
RT      "The complete sequence of the 1.683-kb PSYMB megaplasmid from the N2-
RT      fixing endosymbiont Sinorhizobium meliloti."
RL      Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
DR      EMBL; AL603646; CAC49629.1; -
KW      Plasmid; Hypothetical protein; Complete proteome.
SQ      SEQUENCE 387 AA; 39149 MW; 759202216369F18E CRC64;

Query Match      64.9%; Score 50; DB 16; Length 387;
Best Local Similarity 69.2%; Pred. No. 1.6;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY      2 NDFIFHSGEGDDL 14
      1111 11111 :1:1 :
Db      81 NDFIFGEGENDYL 93

RESULT 12
ID      051868      PRELIMINARY;      PRT;      208 AA.
AC      051868; 051866;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      LEUKOTOXIN A (FRAGMENT).

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Mon Sep 16 16:43:31 2002

us-09-884-696-13.rspt

||:| |:| |:|
Db 774 NDLHGKGDPI 785

Search completed: September 11, 2002, 09:01:27
Job time: 285 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 09:01:55 : Search time 22.74 Seconds

(without alignments)
23.838 Million cell updates/sec

Title: US-09-884-696-13

Sequence: 1 FNDIFHSGEGDDL 14

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	76.6	1050	LKTA_ACTAC	P16462 actinobacil
2	58	75.3	1049	RT31_ACTPL	P55130 actinobacil
3	58	75.3	1052	RT32_ACTPL	P55131 actinobacil
4	56	72.7	1024	HLVA_ECOLI	P08715 escherichia
5	49	63.6	953	LKAI_PASHA	P16535 pasteurella
6	49	63.6	953	LKAB_PASHA	P55118 pasteurella
7	49	63.6	953	LKAA_PASHA	P55117 pasteurella
8	49	63.6	1023	RT11_ACTPL	P55128 actinobacil
9	48	62.3	1023	RT12_ACTPL	P55129 actinobacil
10	46	59.7	284	NODO_RHIV	P09983 escherichia
11	46	59.7	956	HLVA_ACTSU	P15728 rhizobium 1
12	46	59.7	956	HLVA_ACTSU	P00951 actinobacil
13	46	59.7	956	RT2A_ACTPL	P15377 actinobacil
14	45	58.4	947	LKTA_PASSP	P55123 pasteurella
15	42.5	55.2	491	ZAPA_PROMI	P11137 proteus mir
16	42	54.5	953	LKAI_PASHA	P55116 pasteurella
17	42	54.5	1705	CYAA_BORBR	P57506 bordetella
18	42	54.5	1706	CYAA_BORPE	P15318 bordetella
19	41	53.2	503	AK10_MOUSE	O08845 mus musculus
20	41	53.2	650	AK10_PIG	P57770 sus scrofa
21	41	53.2	662	AK10_HUMAN	O43572 homo sapien
22	41	53.2	1829	FRPC_NEIMC	P55127 neisseria m
23	40	51.9	213	ERAC_HUMAN	O43821 homo sapien
24	40	51.9	2327	CCAB_MOUSE	O55017 mus musculus
25	40	51.9	2336	CCAB_RAT	O02294 ratus norv
26	40	51.9	2339	CCAB_HUMAN	O00975 homo sapien
27	39	50.6	547	YM30_YEAST	O03795 saccharomyc
28	39	50.6	628	ABRA_ASPIG	P42554 aspergillus
29	39	50.6	853	PXA2_YEAST	P34330 saccharomyc
30	39	50.6	875	FOCD_ECOLI	P46009 escherichia
31	38	49.4	1829	FRPC_NEIMB	O94605 neisseria m
32	38	49.4	87	YD63_ARCFU	O28808 archaeoglob
33	38	49.4	113	YD16_SCHPO	O10239 schizosacch

34	38	49.4	282	1	CAPA_CAEL	P34685 caenorhabdi
35	38	49.4	354	1	ALF_CAMJE	P53818 campylobact
36	38	49.4	560	1	J160_HORVU	O00531 hordium vul
37	38	49.4	649	1	MERY_YEAST	O04533 saccharomyc
38	38	49.4	748	1	CLPE_LACIC	O95522 lactococcus
39	38	49.4	1115	1	FRPA_NEIMC	O58092 methanococ
40	38	49.4	1302	1	FRPA_NEIMB	O940K9 neisseria m
41	37.5	48.7	316	1	TKTC_METJA	O58092 methanococ
42	37.5	48.7	795	1	ION_MYCCE	P47481 mycoplasma
43	37	48.1	330	1	PHLC_STRAU	P09978 staphylococ
44	37	48.1	354	1	NODA_MOUSE	P43021 mus musculus
45	37	48.1	455	1	SYS_PYRAB	Q9u221 pyrococcus

ALIGNMENTS

RESULT	ID	Sequence	Standard	PRT	Length
1	LKTA_ACTAC	STANDARD:	PRT: 1050 AA.		
AC	P16462:				
DT	01-AUG-1990 (Rel. 15, Created)				
DT	01-AUG-1990 (Rel. 15, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	Leukotoxin.				
GN	LKTA OR LTA.				
OS	Actinobacillus actinomycetemcomitans (Haemophilus				
OS	actinomycetemcomitans).				
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;				
OC	Actinobacillus.				
OX	NCBI_TaxID=714;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRATN-JP2:				
RX	MEDLINE=89359382; PubMed=2670940;				
RA	Lally E.T., Golub E.E., Kleba I.R., Faichman N.S., Rosenbloom J.,				
RA	Rosenbloom J.C., Gibson C.W., Demuth D.R.;				
RT	Analysis of the Actinobacillus actinomycetemcomitans leukotoxin				
RT	gene. Delineation of unique features and comparison to homologous				
RT	toxins. "				
RT	J. Biol. Chem. 264:15451-15456(1989).				
CC	-1- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A. ACTINOMYCETEMCOMITANS				
CC	MIGHT BE A CYTOTOXIN. POSSIBLY THE MEMBRANE-BOUND HEMOLYSIN.				
CC	-1- SUBCELLULAR LOCATION: OUTER-MEMBRANE ASSOCIATED OR SECRETED (BY				
CC	SIMILARITY).				
CC	-1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING				
CC	CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC				
CC	ACTIVITY.				
CC	-1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE				
CC	INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).				
CC	-1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN				
CC	MODIFIED (BY SIMILARITY).				
CC	-1- DISEASE: ITS TARGET CELL SPECIFICITY IS RESTRICTED TO HUMAN AND				
CC	SOME NON-HUMAN CELLS OF THE MONOMYELOCYTIC LINEAGE.				
CC	-1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.				
CC	-----				
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CC	or send an email to license@sib-sib.ch).				
CC	-----				
CC	EMBL: M27399; AAA21922.1; -				
CC	PIR: B34345; B34345.				
CC	HSSP: P04002; 1WPA.				
CC	InterPro: IPR001343; Hemlysn_Ca_bind.				
CC	InterPro: IPR003355; RTX_N.				
CC	InterPro: IPR003355; RTX_N.				
CC	Pfam: PF00335; hemolysinCbind; 3.				
CC	Pfam: PF02382; RTX; 1.				
CC	PRINTS: PR00313; CABNDNGRPT.				

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DR PRINTS; PR01488; RTXTOXINA.
DR PROSITE; PS00330; HEMOLYSIN.CALCIUM; 5.
KW Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
KW Transmembrane; Lipoprotein; Palmitate.
FT TRANSMEM 339 359
FT TRANSMEM 408 429
FT TRANSMEM 477 501
FT DOMAIN 722 844
FT REPEAT 722 727
FT REPEAT 731 736
FT REPEAT 740 745
FT REPEAT 749 754
FT REPEAT 758 763
FT REPEAT 767 772
FT REPEAT 776 781
FT REPEAT 785 790
FT REPEAT 794 799
FT REPEAT 803 808
FT REPEAT 812 817
FT REPEAT 821 826
FT REPEAT 830 835
FT REPEAT 839 844
SQ SEQUENCE 1050 AA; 114194 MW; 38DF9AA24649F662 CRC64;

Query Match 76.6%; Score 59; DB 1; Length 1050;
Best Local Similarity 64.3%; Pred. No. 0.032; Mismatches 0; Gaps 0;
Matches 9; Conservative 3; Indels 2;

OY 1 FNDIFHSGEDDL 14
Db 734 FNDVFHGDGDLI 747

RESULT 2
RT31_ACRPL STANDARD; PRT; 1049 AA.
AC P55130;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RTX-III toxin determinant A from serotype 2 (APX-IIIA) (Cytolysin
DE IIA) (GLY-IIIA).
GN APXIIIA OR CIIITIA OR RTXA OR PTXA.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OX NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROTYPE 2;
RX MEDLINE-93263992; PubMed=8494611;
RA Chang Y.-F., Shi J., Ma D.-P., Shin S.J., Lein D.H.;
RT "Molecular analysis of the Actinobacillus pleuropneumoniae RTX
RT toxin-III gene cluster.";
RL DNA Cell Biol. 12:351-362(1993).
[2]
RN SEQUENCE OF 828-1049 FROM N.A.
RP STRAIN-1536 / SEROTYPE 2;
RX MEDLINE-95012630; PubMed=7927703;
RA Jansen R., Briatore J., van Geel A.B.M., Kamp E.M., Gielkens A.L.J.,
RA Smits M.A.;
RT "Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (ApX)
RT operons: characterization of the ApXIII operons.";
RL Infect. Immun. 62:4411-4418(1994).
CC -1- FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY BUT SHOWS A STRONG
CC CYTOTOXICITY TOWARDS ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY (BY SIMILARITY).
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).

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CC -1- PTM: PALMITOYLATED BY APXIIIC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; I12145; AAA1924.1; ALT_SEQ.
DR EMBL; X80056; CAB37652.1; ALT_Ca_bind.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003395; RTX_N.
DR InterPro: IPR003995; RTX_A.
DR Pfam; PF00353; hemolysinCabin; 2.
DR Pfam; PF02382; RTX; 1.
DR PRINTS; PR00313; CABDNCRPT.
DR PRINTS; PR01488; RTXTOXINA.
DR PROSITE; PS00330; HEMOLYSIN.CALCIUM; 3.
KW Toxin; Cytolysis; Cytotoxin; Repeat; Calcium; Transmembrane;
KW Lipoprotein; Palmitate.
FT TRANSMEM 154 170
FT TRANSMEM 315 331
FT TRANSMEM 397 413
FT DOMAIN 753 858
FT REPEAT 753 758
FT REPEAT 762 767
FT REPEAT 771 776
FT REPEAT 780 785
FT REPEAT 789 794
FT REPEAT 798 803
FT REPEAT 807 812
FT REPEAT 826 831
FT REPEAT 835 840
FT REPEAT 844 849
FT REPEAT 853 858
SQ SEQUENCE 1049 AA; 112491 MW; P99846BFD45CE72 CRC64;

Query Match 75.3%; Score 58; DB 1; Length 1049;
Best Local Similarity 71.4%; Pred. No. 0.047;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEDDL 14
Db 747 FNDVFHGDGDLI 760

RESULT 3
RT32_ACRPL STANDARD; PRT; 1052 AA.
AC P55131;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RTX-III toxin determinant A from serotype 8 (APX-IIIA) (Cytolysin
DE IIA) (GLY-IIIA).
GN APXIIIA OR CIIITIA OR RTXA OR PTXA.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OX NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-405 / SEROTYPE 8;
RX MEDLINE-95012630; PubMed=7927703;
RA Jansen R., Briatore J., van Geel A.B.M., Kamp E.M., Gielkens A.L.J.,
RA Smits M.A.;
RT "Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (ApX)
RT operons: characterization of the ApXIII operons.";

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RL Infect. Immun. 62:4411-4418(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROTYPE 8;
RX MEDLINE-9316286; PubMed-8432615;
RA Jansen R., Briatire J., Kamp E.M., Gielkens A.L.J., Smits M.A.;
RT "Cloning and characterization of the Actinobacillus
RT pleuropneumoniae-RTX-toxin III (ApxIII) gene.";
RL Infect. Immun. 61:947-954(1993).
CC -1- FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY BUT SHOWS A STRONG
CC CYTOTOXICITY TOWARDS ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY (BY SIMILARITY).
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PTM: PALMITOYLATED BY APMIIC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X80055; CAA56358.1; -
CC DR EMBL: X68815; CAA48711.1; -
CC DR InterPro: IPR001343; Hemlysn_Ca_bind.
CC DR InterPro: IPR003355; RTX_N.
CC DR InterPro: IPR003395; RTXa.
CC DR Pfam: PF00353; hemolysinCbind; 2.
CC DR Pfam: PF02382; RTX; 1.
CC DR PRINTS: PR00313; CABDNCRPT.
CC DR PRINTS: PR01488; RTXTOXINA.
CC DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 3.
CC KW Toxin; Cytolysis; Cytotoxin; Repeat; Calcium; Transmembrane;
CC Lipoprotein; Palmitate.
CC KW TRANSMEM 248 265 POTENTIAL.
CC FT TRANSMEM 275 334 POTENTIAL.
CC FT TRANSMEM 372 418 POTENTIAL.
CC FT DOMAIN 754 859 7 X REPEATS, GLY-RICH.
CC FT REPEAT 754 759 1.
CC FT REPEAT 763 768 2.
CC FT REPEAT 772 777 3.
CC FT REPEAT 781 786 4.
CC FT REPEAT 790 795 5.
CC FT REPEAT 799 804 6.
CC FT REPEAT 808 813 7.
CC FT REPEAT 827 832 8.
CC FT REPEAT 841 841 9.
CC FT REPEAT 845 850 10.
CC FT REPEAT 854 859 11.
CC SQ SEQUENCE 1052 AA; 112809 MW; F83AFEE25A6FD8758 CRC64;

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Query Match 75.3%; Score 58; DB 1; Length 1052;
 Best Local Similarity 71.4%; Pred. No. 0.047;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 ENDIFHSGEDLL 14
 1 1111 :11111
 Db 748 FRDIFHGADGDDL 761

RESULT 4
 ID HLVA_ECOLI STANDARD; PRT; 1024 AA.
 AC P08715;
 DT 01-JAN-1988 (Rel. 06, Created)

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DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DR Hemolysin, plasmid.
GN HLVA.
OS Escherichia coli.
OG Plasmid Inc12 PHX152.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Hess J., Wels W., Vogel M., Goebel W.;
RT "Nucleotide sequence of a plasmid-encoded hemolysin determinant and
RT its comparison with a corresponding chromosomal hemolysin sequence.";
RL FEMS Microbiol. Lett. 34:1-11(1986).
RN [2]
RP PALMITOYLATION OF LYS-564 AND LYS-690.
RX MEDLINE-95099325; PubMed-7801126;
RA Stanley P., Packman L.C., Koronakis V., Hughes C.;
RT "Fatty acylation of two internal lysine residues required for the
RT toxic activity of Escherichia coli hemolysin.";
RL Science 266:1992-1996(1994).
RN [3]
RP PALMITOYLATION OF LYS-564 AND LYS-690.
RX MEDLINE-96404790; PubMed-8808931;
RA Ludwig A., Garcia F., Bauer S., Jarchau T., Benz R., Hoppe J.,
RA Goebel W.;
RT "Analysis of the in vivo activation of hemolysin (HLVA) from
RT Escherichia coli.";
RL J. Bacteriol. 178:5422-5430(1996).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.
CC -1- PTM: PALMITOYLATED BY HLC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED.
CC -1- DISEASE: THE HEMOLYSIN OF E. COLI IS PRODUCED PREDOMINANTLY BY
CC STRAINS CAUSING EXTRAINTestinal INFECTIONS, SUCH AS THOSE OF THE
CC URINARY TRACT.
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M14107; AAA98233.1; -
CC DR InterPro: IPR001343; Hemlysn_Ca_bind.
CC DR InterPro: IPR003355; RTX_N.
CC DR InterPro: IPR003395; RTXa.
CC DR Pfam: PF00353; hemolysinCbind; 2.
CC DR Pfam: PF02382; RTX; 1.
CC DR PRINTS: PR00313; CABDNCRPT.
CC DR PRINTS: PR01488; RTXTOXINA.
CC DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4. Repeat; Calcium;
CC Hemolysis; Toxin; Cytolysis; Cytotoxin; Palmitate; Plasmid.
CC KW Transmembrane; Lipoprotein;
CC KW TRANSMEM 238 260 POTENTIAL.
CC FT TRANSMEM 268 327 POTENTIAL.
CC FT TRANSMEM 365 411 POTENTIAL.
CC FT DOMAIN 724 870 16 X REPEATS, GLY-RICH.
CC FT REPEAT 724 729 1.
CC FT REPEAT 733 738 2.
CC FT REPEAT 742 747 3.
CC FT REPEAT 751 756 4.

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CC	-1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/).
CC	or send an email to license@isb-sib.ch .
DR	EMBL; M20730; AAA25529.1; -.
DR	EMBL; M24197; AAA25543.1; -.
DR	PIR; S29516; S29516.
DR	HSSP; P02392; ICTF.
DR	InterPro; IPR001343; Hemlysn_Ca_bind.
DR	InterPro; IPR003355; RTX_N.
DR	InterPro; IPR003995; RTX_A.
DR	Pfam; PF00353; hemolysincabind; 1.
DR	Pfam; PF02382; RTX_1.
DR	PRINTS; PR00313; CANNONCRPT.
DR	PRINTS; PR01488; RIXTOXINA.
KW	PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 4.
KW	Hemolysis; Toxin; Cytolysis; Cytolextin; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate.
KW	TRANSMEM 229 249 POTENTIAL.
FT	TRANSMEM 297 318 POTENTIAL.
FT	DOMAIN 734 784 6 X REPEATS, GLY-RICH (BY SIMILARITY).
FT	REPEAT 734 739 1.
FT	REPEAT 743 748 2.
FT	REPEAT 752 757 3.
FT	REPEAT 761 766 4.
FT	REPEAT 770 775 5.
FT	REPEAT 779 784 6.
FT	CONFLICT 409 414 PEHVAN -> ISTIQI (IN REF. 2).
FT	CONFLICT 742 742 D-> Y (IN REF. 2).
SQ	SEQUENCE 953 AA; 101996 MW; F793D113A118C05F CRC64;
Query Match	63.6%; Score 49; DB 1; Length 953;
Best Local Similarity	58.3%; Pred. No. 1.4;
Matches 7; Conservative	3; Mismatches 2; Indels 0; Gaps 0
OY	2 NDIHSGEGDDL 13 Db 774 NDLLHGKGDDI 785
RESULT 6	
LKAB_PASHA	STANDARD; PRT; 953 AA.
ID LKAB_PASHA	P55118;
AC	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	Leukotoxin from serotype A11.
GN	Lkta.
OS	Pasteurella haemolytica.
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC	Mannheimia.
OX	NCBI_TaxID=75985;
RN	(1)
RP	SEQUENCE FROM N.A.
RC	STRAIN-SEROTYPE A11;
RX	MEDLINE=94041617; PubMed=8225575;
RA	Burrows L.V., Olah-Walfield E., Io R.Y.C.;
RT	"Molecular analysis of the leukotoxin determinants from Pasteurella haemolytica serotypes 1 to 16".
RL	Infect. Immun. 61:5001-5007(1993).
CC	-1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELLS MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
CC	-1- SUBCELLULAR LOCATION: Secreted.

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CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U01215; AAB36689.1; -
CC InterPro: IPR001343; HemLysn_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC InterPro: IPR003995; RtxA.
CC Pfam: PF00353; hemolysinCbind; 1.
CC Pfam: PF02382; RTX_1.
CC PRINTS: PR00313; CABNDNGRPT.
CC PRINTS: PR01488; RTXTOXIN.
CC PROSITE: PS00330; HEMOLYSIN_CALCITUM; 4.
CC Hemolysins; Toxin; Cytolysis; Cytolextin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; Palmitate.
CC TRANSMEM 230 250
CC TRANSMEM 297 317
CC TRANSMEM 381 401
CC TRANSMEM 734 784
CC DOMAIN 734 739
CC REPEAT 734 739
CC REPEAT 743 748
CC REPEAT 752 757
CC REPEAT 761 766
CC REPEAT 770 775
CC REPEAT 779 784
CC REPEAT 781 786
CC SEQUENCE 953 AA; 102206 MW; 927FF56CFC84F12 CRC64;

Query Match 63.6%; Score 49; DB 1; Length 953;
Best Local Similarity 58.3%; Pred. No. 1.4;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHFSGEGDDL 13
Db 774 NDLLHGKGDDI 785

RESULT 7
LKAA_PASHA STANDARD; PRT; 955 AA.
ID LKAA_PASHA
AC P5117;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Leukotoxin from serotype T10.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OC NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-SEROTYPE T10;
RX MEDLINE-96425875; Pubmed-8828217;
RA Lainson F.A., Murray J., Davies R.C., Donachie W.;
RT "Characterization of epitopes involved in the neutralization of
RT Pasteurella haemolytica serotype A1 leukotoxin.";
RL Microbiology 142:2499-2507(1996).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
```

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CC DEFINED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC -----
CC EMBL: Z26247; CAA81206.1; -
CC InterPro: IPR001343; HemLysn_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC InterPro: IPR003995; RtxA.
CC Pfam: PF00353; hemolysinCbind; 1.
CC Pfam: PF02382; RTX_1.
CC PRINTS: PR00313; CABNDNGRPT.
CC PRINTS: PR01488; RTXTOXIN.
CC PROSITE: PS00330; HEMOLYSIN_CALCITUM; 4.
CC Hemolysins; Toxin; Cytolysis; Cytolextin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; Palmitate.
CC TRANSMEM 299 319
CC TRANSMEM 361 381
CC TRANSMEM 736 786
CC DOMAIN 736 786
CC REPEAT 736 741
CC REPEAT 745 750
CC REPEAT 754 759
CC REPEAT 763 768
CC REPEAT 772 777
CC REPEAT 781 786
CC SEQUENCE 955 AA; 102187 MW; B60F2DB8168BCAF CRC64;

Query Match 63.6%; Score 49; DB 1; Length 955;
Best Local Similarity 58.3%; Pred. No. 1.4;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHFSGEGDDL 13
Db 776 NDLLHGKGDDI 787

RESULT 8
RTLL_ACPPL STANDARD; PRT; 1023 AA.
ID RTLL_ACPPL
AC P5128;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RTX-I toxin determinant A from serotypes 1/9 (APX-1A) (Hemolysin IA)
DE (HLX-1A) (Cytolysin IA) (CLY-1A).
GN APXIA OR CLYIA OR HLXIA.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OC NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-S 4074 / SEROTYPE 1;
RX MEDLINE-91348845; Pubmed-1879928;
RA Frey J., Meier R., Gysi D., Nicolet J.;
RT "Nucleotide sequence of the hemolysin I gene from Actinobacillus
RT pleuropneumoniae.";
```

RL Infect. Immun. 59:3026-3032(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S 4074 / SEROTYPE 1;
 RX MEDLINE=94237497; PubMed=8181764;
 RA Frey J., Haidemann A., Nicolet J., Boffini A., Prentki P.;
 RT "Sequence analysis and transcription of the apxi operon (hemolysin I)
 RL from *Actinobacillus pleuropneumoniae*." Gene 142:97-102(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ISOLATE CVI 13261 / SEROTYPE 9;
 RX MEDLINE=93366425; PubMed=8359891;
 RA Jansen R., Briatare J., Kamp E.M., Gielkens A.L.J., Smits M.A.;
 RT "Structural analysis of the *Actinobacillus pleuropneumoniae*-RTX-toxin
 RL Infect. Immun. 61:3688-3695(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S 4074 / SEROTYPE 1;
 RA Chang Y., Wang Y., Chin N.;
 RL Submitted (JUN-1994) to the VIRULENCE FACTORS OF *A. PLEUROPNEUMONIAE*,
 CC -1- FUNCTION: ONE OF THE VIRULENCE FACTORS OF *A. PLEUROPNEUMONIAE*,
 CC WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTOXIC FOR
 CC ALVEOLAR MACROPHAGES AND NEUTROPHILS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 CC ACTIVITY.
 CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
 CC -1- PTM: PALMITOYLATED BY APXIC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 CC MODIFIED (BY SIMILARITY).
 CC -1- MISCELLANEOUS: APXIA IS PARTIALLY DELETED IN SEROTYPES 2, 4, 6, 7,
 CC 8, 12, AND TOTALLY DELETED IN SEROTYPE 3.
 CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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 CC
 CC EMBL: X52899; CAA37081.1; -
 CC EMBL: X68595; CAA48596.1; -
 CC EMBL: X73117; CAA51548.1; -
 CC EMBL: U05042; AAB05034.1; -
 CC DR EMBL: IPR001343; Hemlysn_Ca_bind.
 CC DR InterPro: IPR003355; RTX_N.
 CC DR InterPro: IPR003995; RTXA.
 CC DR Pfam: PF00353; hemolysincabind; 2.
 CC DR Pfam: PF02382; RTX; 1.
 CC DR PRINTS: PR00313; CABDNCRPT.
 CC DR PRINTS: PR01488; RTXTOXINA.
 CC DR PROSITE: PS00330; HEMOLYSIN-CALCIUM; 2.
 CC KW Hemolysin; Toxin; Cytolysin; Cytolextin; Repeat; Calcium;
 CC Transmembrane; Lipoprotein; Palmitate.
 CC FT TRANSMEM 226 256
 CC FT TRANSMEM 297 326
 CC FT TRANSMEM 367 406
 CC FT DOMAIN 722 845
 CC FT REPEAT 722 727
 CC FT REPEAT 731 736
 CC FT REPEAT 740 745
 CC FT REPEAT 749 754
 CC FT REPEAT 758 763
 CC FT REPEAT 767 772
 CC FT REPEAT 776 781
 CC FT REPEAT 785 790
 CC FT REPEAT 794 799

FT REPEAT 813 818 10.
 FT REPEAT 822 827 11.
 FT REPEAT 831 836 12.
 FT REPEAT 840 845 13.
 FT CONFLICT 210 217
 FT CONFLICT 374 374 R -> A (IN REF. 3 AND 4).
 FT CONFLICT 562 562 Q -> E (IN REF. 3 AND 4).
 FT CONFLICT 687 687 TC -> R (IN REF. 3 AND 4).
 SQ SEQUENCE 1023 AA; 110193 MW; F99A88CFC9F1A598 CRC64;

 Query Match 63.6%; Score 49; DB 1; Length 1023;
 Best Local Similarity 66.7%; Pred. No. 1.6;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 Oy 1 FNDFHSGGDD 12
 Db 734 FTDFHAGKGD 745

 RESULT 9
 RT12 ACPL STANDARD; PRT; 1023 AA.
 ID RT12 ACPL
 AC P55129;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 39, Last annotation update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE RTX-I toxin determinant A from serotypes 5/10 (APX-1A) (*Hemolysin IA*)
 DE (HLX-1A) (*Cytolysin IA*) (CLY-1A).
 GN *Actinobacillus pleuropneumoniae* (*Haemophilus pleuropneumoniae*).
 OS *Actinobacillus pleuropneumoniae* (*Haemophilus pleuropneumoniae*).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
 CC *Actinobacillus*.
 OX NCBI_Taxid=715;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-13039 / SEROTYPE 10;
 RX MEDLINE=94276858; PubMed=8007819;
 RA Nagai S., Yagihashi T., Ishihama A.;
 RT "DNA sequence analysis of an allelic variant of the *Actinobacillus*
 RL *pleuropneumoniae*-RTX-toxin I (APXIA) from serotype 10." J.
 RN Microb. Pathog. 15:485-495(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K17 / SEROTYPE 5;
 RX MEDLINE=96401417; PubMed=8807793;
 RA Chin N., Frey J., Chang C.F., Chang Y.F.;
 RT "Identification of a locus involved in the utilization of iron by
 RL *Actinobacillus pleuropneumoniae*." J.
 RN FEMS Microbiol. Lett. 143:1-6(1996).
 RN [3]
 RP SEQUENCE OF 886-1023 FROM N.A.
 RC STRAIN-K17 / SEROTYPE 5;
 RX MEDLINE=93366425; PubMed=8359891;
 RA Jansen R., Briatare J., Kamp E.M., Gielkens A.L.J., Smits M.A.;
 RT "Structural analysis of the *Actinobacillus pleuropneumoniae*-RTX-toxin
 RL I (Apxi) operon." J.
 RN Infect. Immun. 61:3688-3695(1993).
 CC -1- FUNCTION: ONE OF THE VIRULENCE FACTORS OF *A. PLEUROPNEUMONIAE*,
 CC WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTOXIC FOR
 CC ALVEOLAR MACROPHAGES AND NEUTROPHILS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 CC ACTIVITY.
 CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
 CC -1- PTM: PALMITOYLATED BY APXIC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 CC MODIFIED (BY SIMILARITY).
 CC -1- MISCELLANEOUS: APXIA IS PARTIALLY DELETED IN SEROTYPES 2, 4, 6, 7,
 CC 8, 12, AND TOTALLY DELETED IN SEROTYPE 3.
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF SEROTYPE 10.
 CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.

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CC -----
DR EMBL: D16582; BA04014.1; -
DR EMBL: U04954; AAB17220.1; -
DR EMBL: X73116; CAA51546.1; -
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RTX_A.
DR Pfam: PF02382; RTX_1.
DR PRINTS: PR00313; CABDNGRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CYTOTOXIN; Repeat; Calcium;
KW Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
KM Transmembrane; Lipoprotein; Palmitate.
FT TRANSMEM 226 256
FT TRANSMEM 297 326
FT TRANSMEM 367 406
FT DOMAIN 722 845 13 X REPEATS, GLY-RICH.
FT REPEAT 722 727 1.
FT REPEAT 731 736 2.
FT REPEAT 740 745 3.
FT REPEAT 749 754 4.
FT REPEAT 758 763 5.
FT REPEAT 767 772 6.
FT REPEAT 776 781 7.
FT REPEAT 785 790 8.
FT REPEAT 794 799 9.
FT REPEAT 813 818 10.
FT REPEAT 822 827 11.
FT REPEAT 831 836 12.
FT REPEAT 840 845 13.
FT CONFLICT 210 217 AMPYLTLA -> GNAISNTR (IN REF. 2).
FT CONFLICT 581 581 E -> Q (IN REF. 2).
FT CONFLICT 687 688 TC -> R (IN REF. 2).
FT CONFLICT 1015 1015 F -> L (IN REF. 2).
SQ SEQUENCE 1023 AA; 110129 MW; 183C7C15E57DB55 CRC64;

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Query Match 63.6%; Score 49; DB 1; Length 1023;
 Best Local Similarity 66.7%; Pred. No. 1.6;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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OY 1 FNDIFHSGEDD 12
DB 734 FTDIFHGAKGD 745

RESULT 10
ID HLY1_ECOLI STANDARD; PRT: 1023 AA.
AC P09983;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Hemolysin, chromosomal.
GN HLYA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J96 / SEROTYPE O4;
RX MEDLINE=85234404; PubMed=3891743;
RA Feilmee T., Pellett S., Welch R.A.;

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RT "Nucleotide sequence of an Escherichia coli chromosomal hemolysin.";
RL J. Bacteriol. 163:94-105(1985).
RN [2]
RP SEQUENCE OF 1-44 FROM N.A.
RC STRAIN=2001;
RX MEDLINE=85258115; PubMed=3894051;
RA Nicoud J.-M., Mackman N., Gray L., Holland I.B.;
RT "Characterisation of HlyC and mechanism of activation and secretion
RT of haemolysin from E. coli 2001.";
RL FEBS Lett. 187:339-344(1985).
CC -! FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -! SUBCELLULAR LOCATION: Secreted
CC -! DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -! DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.
CC -! PTM: PALMITOYLATED BY HLYC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED.
CC -! DISEASE: THE HEMOLYSIN OF E. COLI IS PRODUCED PREDOMINANTLY BY
CC STRAINS CAUSING EXTRAINTESTINAL INFECTIONS, SUCH AS THOSE OF THE
CC URINARY TRACT.
CC -! SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC -----
DR EMBL: M10133; AAA23975.1; -
DR EMBL: X02768; CAA26546.1; -
DR PIR: A24433; LEECA.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RTX_A.
DR Pfam: PF00353; hemolysinCa_bind.
DR Pfam: PF02382; RTX_1.
DR PRINTS: PR00313; CABDNGRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CYTOTOXIN; Repeat; Calcium;
KW Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
KM Transmembrane; Lipoprotein; Palmitate.
FT TRANSMEM 237 259
FT TRANSMEM 267 326
FT TRANSMEM 364 410
FT DOMAIN 723 869
FT REPEAT 723 728 1.
FT REPEAT 729 734 2.
FT REPEAT 732 737 3.
FT REPEAT 741 746 4.
FT REPEAT 750 755 5.
FT REPEAT 759 764 6.
FT REPEAT 768 773 7.
FT REPEAT 772 777 8.
FT REPEAT 776 781 9.
FT REPEAT 786 791 10.
FT REPEAT 795 800 11.
FT REPEAT 806 812 12.
FT REPEAT 816 821 13.
FT REPEAT 825 830 14.
FT REPEAT 834 839 15.
FT REPEAT 843 848 16.
FT REPEAT 855 860 17.
FT REPEAT 864 869 18.
FT LIPID 563 563 PALMITATE (BY SIMILARITY).
FT LIPID 689 689 PALMITATE (BY SIMILARITY).
FT VARIANT 6 6 A -> T (IN STRAIN 2001).
SQ SEQUENCE 1023 AA; 109867 MW; 196D5C0A9A28B54D CRC64;

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DR InterPro: IPR003355; RTX_N.
 DR InterPro: IPR003995; RtxA.
 DR Pfam: PF00353; hemolysincabind; 1.
 DR Pfam: PF02382; RTX_1.
 DR PRINTS: PR00313; CABDNGRPT.
 DR PRINTS: PR01488; RTXTOXINA.
 DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4.
 DR Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
 KM Transmembrane; Lipoprotein; Palmitate.
 FT TRANSMEM 154 170 POTENTIAL.
 FT TRANSMEM 312 333 POTENTIAL.
 FT TRANSMEM 393 414 POTENTIAL.
 FT DOMAIN 625 780 7 X REPEATS, GLY-RICH.
 FT REPEAT 625 630 1.
 FT REPEAT 730 735 2.
 FT REPEAT 739 744 3.
 FT REPEAT 748 753 4.
 FT REPEAT 757 762 5.
 FT REPEAT 766 771 6.
 FT REPEAT 775 780 7.
 SQ SEQUENCE 947 AA; 101559 MW; 9744F06395EF5BED CRC64;

Query Match 58.4%; Score 45; DB 1; Length 947;
 Best Local Similarity 53.8%; Pred. No. 6.9;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 2 NDIHSGEGDDL 14
 Db 770 DDILHGKGNL 782

RESULT 15
 ZAPA_PROMI STANDARD; PRT: 491 AA.
 AC Q1137;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Extracellular metalloprotease precursor (EC 3.4.24.-).
 GN ZAPA.
 OS Proteus mirabilis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Proteus.
 OX NCBL_TaxID=584;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BB2000;
 RX MEDLINE-96011363; PubMed-7592325;
 RA Wassif C., Cheek D., Belas R.;
 RT "Molecular analysis of a metalloprotease from proteus mirabilis."
 RL J. Bacteriol. 177:5790-5798(1995).
 CC -1- FUNCTION: ONE OF THE VIRULENCE FACTORS PRODUCED DURING SWARMER
 CELL DIFFERENTIATION OF THE BACTERIA. WHICH SEEMS TO BE ASSOCIATED
 WITH PATHOGENESIS. THE PROTEASE ACTIVITY IS LIMITED TO IG A1,
 IG A2, AS WELL AS IG G DEGRADATION.
 CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
 CC -1- ENZYME REGULATION: CA2+ INCREASES PROTEASE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: THE GLY-RICH REPEATS MAY BE IMPORTANT IN THE
 EXTRACELLULAR SECRETION OF THIS METALLOPROTEASE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10B (ZINC
 METALLOPROTEASE); ALSO KNOWN AS THE SERRALYSIN SUBFAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U25950; AAA86729.1; ALT_INIT.

DR HSSP: P23694; 1SAT.
 DR MEROPS: M10.057; -.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR000130; Zn_Mtpeptidse.
 DR Pfam: PF00353; hemolysincabind; 1.
 DR PRINTS: PR00313; CABDNGRPT.
 DR SMART: SM00235; zmc; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; FALSE NEG.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KM Hydrolyse; Metalloprotease; Zinc; Zymogen; Repeat; Virulence; Calcium.
 FT PROPEP 1 16 POTENTIAL.
 FT CHAIN 17 491 EXTRACELLULAR METALLOPROTEASE.
 FT METAL 186 186 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT SITE 187 187 BY SIMILARITY.
 FT METAL 190 190 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 196 196 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 226 226 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DOMAIN 343 393 4 X REPEATS, GLY-RICH.
 FT REPEAT 343 348 1.
 FT REPEAT 361 366 2.
 FT REPEAT 379 384 3.
 FT REPEAT 388 393 4.
 SQ SEQUENCE 491 AA; 54000 MW; 1E6DEE3F6243A97 CRC64;

Query Match 55.2%; Score 42.5; DB 1; Length 491;
 Best Local Similarity 40.9%; Pred. No. 8.9;
 Matches 9; Conservative 2; Mismatches 2; Indels 9; Gaps 1;
 QY 2 NDIH-----SGEGDDL 14
 Db 347 NDIHGNADNDTLGEGDDII 368

Search completed: September 11, 2002, 09:01:55
 Job time: 278 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 09:00:14 : Search time 40.83 Seconds
(without alignments)
32.948 Million cell updates/sec

Title: US-09-884-696-13
Perfect score: 77
Sequence: 1 FNDIFHSGECDLL 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	76.6	1055	1 A37205	Leukotoxin A - Act
2	58	75.3	1049	1 S51784	Leukotoxin III - Actino
3	58	75.3	1052	1 B49219	Leukotoxin III - Actino
4	56	72.7	1024	2 S10056	hemolysin A - Esch
5	52	67.5	998	2 I41078	hemolysin A - Escher
6	52	67.5	998	2 T00227	hemolysin A toxin
7	52	67.5	998	2 AH2137	hypothetical prote
8	50	64.9	387	2 E95995	hypothetical calci
9	49	63.6	208	2 S34238	Leukotoxin A - Pas
10	49	63.6	208	1 B30169	Leukotoxin A - Pas
11	49	63.6	955	1 A35254	Leukotoxin A - Pas
12	49	63.6	1022	1 I39643	Leukotoxin A - Pas
13	48	62.3	334	2 E69361	signal transducing
14	48	62.3	1023	1 LEECA	hemolysin A - Esch
15	47	61.0	302	2 AD2546	hypothetical prote
16	47	61.0	1417	2 AG2137	hypothetical prote
17	46	59.7	284	2 S08385	nodal protein - Rhl
18	46	59.7	284	2 A43721	nodal protein - Rhl
19	46	59.7	644	2 C95991	conserved hypotet
20	46	59.7	956	1 B33389	conserved hypotet
21	46	59.7	956	1 A43834	toxins II - Actinob
22	45	58.4	1771	2 S76851	toxins II - Actinob
23	43	55.8	219	2 B95953	hypothetical prote
24	43	55.8	1112	2 H95964	probable outer mem
25	42	54.5	282	2 F90077	conserved hypotet
26	42	54.5	395	2 T00574	probable protein K
27	42	54.5	539	2 G95405	hypothetical prote
28	42	54.5	591	2 S74999	iron-regulated pro
29	42	54.5	650	2 G87572	calcium-binding pr

30	42	54.5	1208	2 C82779	hemolysin-type cal
31	42	54.5	1254	2 G86379	protein F5A9.24 [1
32	42	54.5	1706	1 OYBRC	cycloleucin - Borde
33	42	54.5	1741	2 S74910	hemolysin - Synech
34	42	54.5	2064	2 G82562	Dactylocten afe2407
35	41	53.2	143	2 T13214	minor capsid prote
36	41	53.2	218	2 H84328	3-phosphoglycerate
37	41	53.2	319	2 F82348	hypothetical prote
38	41	53.2	387	2 E95933	probable calcium-b
39	41	53.2	681	2 AB2155	hypothetical prote
40	41	53.2	826	2 AB1841	hypothetical prote
41	41	53.2	993	2 AE1905	outer membrane sec
42	41	53.2	1072	2 G95851	probable hemolysin
43	41	53.2	1290	2 S76853	hypothetical prote
44	41	53.2	1403	2 S77624	mannuronan C-5-epi
45	41	53.2	1705	2 S51672	adenylate cyclase

ALIGNMENTS

RESULT 1
A37205
Leukotoxin A - Actinobacillus actinomycetemcomitans
C:Species: Actinobacillus actinomycetemcomitans
C:Date: 16-Sep-1992 #sequence-revision 01-Nov-1996 #text-change 31-Mar-2000
C:Accession: A37205; A60768; B34345; A32276; PH0267; PH0266; S17284
R:Kraly, E.; Dailey, T.; Kolodrubetz, D.
Infect. Immun. 58, 920-929, 1990
A:Title: Nucleotide sequence of the leukotoxin gene from Actinobacillus actinomycetemcomitans
A:Reference number: A37205; M01D:90202154
A:Accession: A37205
A:Molecule type: DNA
A:Residues: 1-1055 <KRA>
A:Cross-references: GB:X16829; M1D:938643; P1D:CAA34731.1; P1D:938645
A:Note: The authors present evidence that the nucleotide sequence is correct in the v
sing nucleotide
R:Kolodrubetz, D.; Dailey, T.; Ebersole, J.; Kraly, E.
Infect. Immun. 57, 1465-1469, 1989
A:Title: Cloning and expression of the leukotoxin gene from Actinobacillus actinomycetemcomitans
A:Reference number: A60768; M01D:89212893
A:Accession: A60768
A:Molecule type: DNA
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Residues: 297-309, 'Y', 311-364, 434-440, 'KC', 443-474, 'H', 476-489, 'S', 491-493, 'VLK', 49
A:Note: This sequence is revised in reference A37205
R:Kraly, E.T.; Golub, E.E.; Kleba, I.R.; Talchman, N.S.; Rosenbloom, J.; Rosenbloom, J.
J. Biol. Chem. 264, 15451-15456, 1989
A:Title: Analysis of the Actinobacillus actinomycetemcomitans leukotoxin gene. Delin
A:Reference number: A34345; M01D:89359382
A:Accession: B34345
A:Molecule type: DNA
A:Residues: 1-239, 'Y', 241-259, 'H', 261-335, 'A', 337-415, 'S', 417-438, 'S', 440-723, 'N', 725
PVRKPRHRCRPLTITLTIQIR' <LAL>
A:Cross-references: GB:M27933
R:Kraly, E.T.; Kleba, I.R.; Demuth, D.R.; Rosenbloom, J.; Golub, E.E.; Talchman, N.S
Biochem. Biophys. Res. Commun. 159, 256-262, 1989
A:Title: Identification and expression of the Actinobacillus actinomycetemcomitans le
A:Reference number: A32276; M01D:89165863
A:Accession: A32276
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 430-438, 'S', 440-476, 'R', 478-506, 'KRS', 511, 'GSAINSLNTD', 523-541, 'I', 543,
A:Note: This sequence is revised in reference A34345
R:Ohta, H.; Miyagi, A.; Kato, K.; Fukui, K.
Submitted to JIPID, July 1995
A:Description: Modulation of leukotoxin production by growth rate and bicarbonate in
A:Reference number: PH0266
A:Accession: PH0267
A:Molecule type: protein
A:Residues: 17-42 <OHT>
A:Experimental source: strain 301-b
A:Accession: PH0266

A:Molecule type: protein
 A:Residues: 2-6, 'L', 8-26 <OH2>
 C:Genetics:
 A:Gene: ltxA
 C:Function:
 A:Description: lyses human polymorphonuclear lymphocytes and monocytes
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: cytotoxins; hemolysins; lipoprotein; periplasmic space; tandem repeat; thioles
 F:245-790/Domain: hemolysin A homology <HLVA>
 F:731-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIVYF]-X)
 F:562,687/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 76.6%; Score 59; DB 1; Length 1055;
 Best Local Similarity 64.3%; Pred. No. 0.088;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FNDIFHSGGDDL 14
 DB 734 FNDIFHSGGDDL 747

RESULT 2
 S51784
 N:toxin III - Actinobacillus pleuropneumoniae (serotype 2)
 N:Alternate names: RTX-toxin IIIA (ApXIIIA)
 C:Species: Actinobacillus pleuropneumoniae
 C>Date: 14-Jul-1995 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
 C:Accession: S51784
 R:Chang, Y.F.; Shih, J.; Ma, D.P.; Shih, S.J.; Lein, D.H.
 DNA Cell Biol. 12, 351-362, 1993
 A:Title: Molecular analysis of the Actinobacillus pleuropneumoniae RTX toxin-III gene cl
 A:Reference number: S51783; MUID:93263992
 A:Accession: S51784
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1049 <CH>
 A:Cross-references: EMBL:L12145; NID:9349605; PIDN:AAA21924.1; PID:9470685
 C:Comment: This organism causes porcine pleuropneumonia.
 C:Genetics:
 A:Gene: apXIIIA
 C:Function:
 A:Description: lyses lung macrophages
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: calcium binding; cytotoxins; exotoxin; lipoprotein; tandem repeat; thiolester
 F:254-803/Domain: hemolysin A homology <HLVA>
 F:735-861/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIVYF]-X)
 F:571,702/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 75.3%; Score 58; DB 1; Length 1049;
 Best Local Similarity 71.4%; Pred. No. 0.13;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGGDDL 14
 DB 747 FNDIFHSGGDDL 760

RESULT 3
 B49219
 N:toxin III - Actinobacillus pleuropneumoniae (serotype 8)
 N:Alternate names: RTX-toxin III (ApXIIIA)
 C:Species: Actinobacillus pleuropneumoniae
 C>Date: 19-Dec-1993 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
 C:Accession: B49219; S48043; S29958
 R:Jansen, R.; Briatore, J.; Kamp, E.M.; Gielkens, A.L.; Smits, M.A.
 Infect. Immun. 61, 947-954, 1993
 A:Title: Cloning and characterization of the Actinobacillus pleuropneumoniae-RTX-toxin I
 A:Reference number: A49219; MUID:93162836
 A:Accession: B49219
 A:Molecule type: DNA
 A:Residues: 1-1052 <JANI>

A:Cross-references: EMBL:X68815; NID:938956; PIDN:CAA48711.1; PID:938958
 A:Experimental source: strain 405, serotype 8
 A>Note: sequence extracted from NCBI backbone (NCBIN:125168, NCBI:P.125170)
 R:Jansen, R.; Briatore, J.; van Geel, A.B.M.; Kamp, E.M.; Gielkens, A.L.J.; Smits, M.A.
 Infect. Immun. 62, 4411-4418, 1994
 A:Title: Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (ApX) operons:
 A:Reference number: S48042; MUID:95012630
 A:Accession: S48043
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1052 <JANI>
 A:Cross-references: EMBL:X60055; NID:9558150; PIDN:CAA56358.1; PID:9558152
 A:Experimental source: strain 405, serotype 8
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
 C:Comment: This organism causes porcine pleuropneumonia.
 C:Genetics:
 A:Gene: apXIIIA
 C:Function:
 A:Description: lyses lung macrophages
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: calcium binding; cytotoxins; exotoxin; lipoprotein; tandem repeat; thioles
 F:254-804/Domain: hemolysin A homology <HLVA>
 F:736-862/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIVYF]-X)
 F:571,702/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 75.3%; Score 58; DB 1; Length 1052;
 Best Local Similarity 71.4%; Pred. No. 0.13;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGGDDL 14
 DB 748 FNDIFHSGGDDL 761

RESULT 4
 S10056
 N:hemolysin A - Escherichia coli plasmid pHLy152
 C:Species: Escherichia coli
 C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 04-Mar-2000
 C:Accession: S10056
 R:Hess, J.; Wels, W.; Vogel, M.; Goebel, W.
 FEMS Microbiol. Lett. 34, 111, 1986
 A:Title: Nucleotide sequence of a plasmid-encoded hemolysin determinant and its compa
 A:Reference number: S07209
 A:Accession: S10056
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1024 <HES>
 A:Cross-references: EMBL:M14107
 C:Genetics:
 A:Genome: plasmid pHLy152
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: lipoprotein
 F:247-792/Domain: hemolysin A homology <HLVA>
 F:564,690/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 72.7%; Score 56; DB 2; Length 1024;
 Best Local Similarity 64.3%; Pred. No. 0.28;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGGDDL 14
 DB 736 FNDIFHSGGDDL 749

RESULT 5
 I41078
 N:hemolysin - Escherichia coli
 C:Species: Escherichia coli
 C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jul-2000
 C:Accession: I41078

R:Schmidt, H.; Beutin, L.; Karch, H.
Infect. Immun. 63, 1055-1061, 1995
A>Title: Molecular analysis of the plasmid-encoded hemolysin of *Escherichia coli* O157:H7
A:Reference number: I41077; PMID:95172699
A:Accession: I41078
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-998 <RES>
A:Cross-references: EMBL:X79839; NID:9860924; PID:CA56234.1; PID:94388764
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: lipoprotein
F:233-776/Domain: hemolysin A homology <HLXA>
F:550,675/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 67.5%; Score 52; DB 2; Length 998;
Best Local Similarity 57.1%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 1 FNDIFHSGGDDL 14
DB 720 FNDIFHSGGNDYI 733

RESULT 6
T00227
hemolysin A toxin protein - *Escherichia coli* plasmid pO157

C:Species: *Escherichia coli*
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C:Accession: T00227; T42148
R:Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, H.C.; Kubota, S.; Shimagawa, H.
DNA Res. 5, 1-9, 1998
A>Title: Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemorrhagic *E. coli* O157:H7
A:Reference number: Z14127; PMID:98290540
A:Accession: T00227
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-998 <MAX>
A:Cross-references: EMBL:AB011549; NID:94589740; PID:BA31774.1; PID:93337015
A:Experimental source: strain EHEC O157:H7, substrain RMD 0509952
R:Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
Nucleic Acids Res. 26, 4196-4204, 1998
A>Title: The complete DNA sequence and analysis of the large virulence plasmid of *Escherichia coli* O157:H7
A:Reference number: Z22066; PMID:98391744
A:Accession: T42148
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-998 <BUR>
A:Cross-references: EMBL:AF074613; PID:NAAC70116.1
A:Experimental source: strain EDL933; serotype O157:H7
C:Genetics:
A:Gene: hlyA
A:Genome: plasmid pO157
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: cytotoxins; hemolysins; lipoprotein; toxin
F:233-776/Domain: hemolysin A homology <HLXA>
F:550,675/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 67.5%; Score 52; DB 2; Length 998;
Best Local Similarity 57.1%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 1 FNDIFHSGGDDL 14
DB 720 FNDIFHSGGNDYI 733

RESULT 7
AH2137
hypothetical protein all2655 [imported] - *Anabaena* sp. (strain PCC 7120)
C:Species: *Anabaena* sp.

A>Note: *Anabaena* sp. (strain PCC 7120) is a synonym of *Nostoc* sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AH2137
R:Kaneke, T.; Nakamura, Y.; Molk, C.P.; Kultz, T.; Sasamoto, S.; Watanabe, A.; Iriy
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A>Title: Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium
A:Reference number: AB1807; PMID:21595285; PMID:11759840
A:Accession: AH2137
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-3262 <KUR>
A:Cross-references: GB:BA000019; PID:BA74354.1; PID:g17131748; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all2655

Query Match 67.5%; Score 52; DB 2; Length 3262;
Best Local Similarity 69.2%; Pred. No. 4.7;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 2 NDIIFHSGGDDL 14
DB 3162 NDIIFHSGGDDL 3174

RESULT 8
E95995

hypothetical calcium binding protein [imported] - *Sinorhizobium meliloti* (strain 1021)
C:Species: *Sinorhizobium meliloti*
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: E95995
R:Finan, T.M.; Weidner, S.; Wong, K.; Bhurmesler, J.; Chain, P.; Vorholter, F.J.; Her
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A>Title: The complete sequence of the 1,683-kb *PSyMB* megaplasmid from the N2-fixing e
A:Reference number: A95842; PMID:21396508; PMID:11481431
A:Accession: E95995
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <KUR>
A:Cross-references: GB:AL591985; PID:CA49629.1; PID:g15141116; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid *PSyMB*
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A>Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; PMID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb21402
A:Genome: plasmid

Query Match 64.9%; Score 50; DB 2; Length 387;
Best Local Similarity 69.2%; Pred. No. 0.99;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 2 NDIIFHSGGDDL 14
DB 81 NDIIFHSGGNDYI 93

RESULT 9
S34238
Leukotoxin A - *Pasteurella haemolytica* (fragment)
N:Alternate names: lktA protein
C:Species: *Pasteurella haemolytica*
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C:Accession: S34238; S34236

R:lainson, A.F.; Aitchison, K.D.; Donachie, W.
 Submitted to the EMBL Data Library, June 1993
 A:Description: DNA sequence of the carboxy terminal end of leukotoxin A from the T4 sero
 of *Pasteurella haemolytica*.
 A:Reference number: S34236
 A:Accession: S34238
 A:Molecule type: DNA
 A:Residues: 1-208 <LA1>
 A:Cross-references: EMBL:Z22885; NID:9311830; PIDN:CAA80499.1; PID:9311831
 A:Experimental source: serotype T4
 A:Accession: S34236
 A:Molecule type: DNA
 A:Residues: 9-208 <LA2>
 A:Cross-references: EMBL:Z22886; NID:9311826; PIDN:CAA80500.1; PID:9311827
 A:Experimental source: serotype T15
 C:Genetics:
 A:Gene: lktA
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
 F:238-784/Domain: hemolysin A homology <HLVA>
 F:716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVLYF]-X)
 F:554/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 63.6%; Score 49; DB 2; Length 208;
 Best Local Similarity 58.3%; Pred. No. 0.74;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDIRHSGEGDDL 13
 ||: ||: ||: ||:
 Db 29 NDLHGGKGGDI 40

RESULT 10
 B30169
 leukotoxin A - *Pasteurella haemolytica* (serotype 1)
 N:Alternate names: lktA protein
 C:Species: *Pasteurella haemolytica*
 C:Date: 12-Oct-1989 #sequence revision 15-Nov-1996 #text_change 18-Jun-1999
 C:Accession: B30169; C32051; S29516
 R:Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstein, G.M.
 DNA 8, 15-28, 1989
 A:Title: DNA sequence of the *Pasteurella haemolytica* leukotoxin gene cluster.
 A:Reference number: A30169; MUID:89210283
 A:Accession: B30169
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-953 <HIG>
 R:Strathdee, C.A.; Lo, R.Y.C.
 J. Bacteriol. 171, 916-928, 1989
 A:Title: Cloning, nucleotide sequence, and characterization of genes encoding the secret
 A:Reference number: A32051; MUID:89123172
 A:Accession: C32051
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 947-953 <STR>
 R:Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E.
 Infect. Immun. 55, 1987-1996, 1987
 A:Title: Nucleotide sequence of the leukotoxin genes of *Pasteurella haemolytica* A1.
 A:Reference number: S29515; MUID:87306837
 A:Accession: S29516
 A:Molecule type: DNA
 A:Residues: 1-741, 'D', 743-953 <LOR>
 A:Cross-references: EMBL:M20730; NID:9150492; PIDN:AAA25529.1; PID:9150494
 C:Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
 C:Genetics:
 A:Gene: lktA
 C:Function:
 A:Description: lyses leukocytes
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
 F:238-784/Domain: hemolysin A homology <HLVA>
 F:716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVLYF]-X)
 F:554/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 63.6%; Score 49; DB 1; Length 953;
 Best Local Similarity 58.3%; Pred. No. 4;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDIRHSGEGDDL 13
 ||: ||: ||: ||:
 Db 774 NDLHGGKGGDI 785

RESULT 11
 A35254
 leukotoxin A - *Pasteurella haemolytica* (serotype T10)
 N:Alternate names: lktA protein
 C:Species: *Pasteurella haemolytica*
 C:Date: 10-Aug-1990 #sequence revision 15-Nov-1996 #text_change 18-Jun-1999
 C:Accession: S37145; A35254; S34237; S34235
 R:lainson, A.F.; Aitchison, K.; Donachie, W.
 submitted to the EMBL Data Library, September 1993
 A:Description: DNA sequence of the leukotoxin A gene from *P. haemolytica* T10 serotype
 A:Reference number: S37145
 A:Accession: S37145
 A:Molecule type: DNA
 A:Residues: 1-955 <LA1>
 A:Cross-references: EMBL:Z26247; NID:9400424; PIDN:CAA81206.1; PID:9400425
 R:Highlander, S.K.; Engler, M.J.; Weinstein, G.M.
 J. Bacteriol. 172, 2343-2350, 1990
 A:Title: Secretion and expression of the *Pasteurella haemolytica* leukotoxin.
 A:Reference number: A35254; MUID:90236888
 A:Accession: A35254
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 950-955 <HIG>
 A:Cross-references: GB:M24197; GB:M34943; GB:M34944
 R:lainson, A.F.; Aitchison, K.D.; Donachie, W.
 submitted to the EMBL Data Library, June 1993
 A:Description: DNA sequence of the carboxy terminal end of leukotoxin A from the T3 s
 A:Reference number: S34235
 A:Accession: S34237
 A:Molecule type: DNA
 A:Residues: 745-955 <LA2>
 A:Cross-references: EMBL:Z22884; NID:9311828; PIDN:CAA80498.1; PID:9311829
 A:Experimental source: serotype T3
 A:Accession: S34235
 A:Molecule type: DNA
 A:Residues: 723-955 <LA3>
 A:Cross-references: EMBL:Z22887; NID:9311824; PIDN:CAA80501.1; PID:9311825
 A:Experimental source: serotype T10
 C:Function:
 A:Description: attacks cell membranes and causes cell lysis
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repe
 F:240-786/Domain: hemolysin A homology <HLVA>
 F:718-809/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVLYF]-X)
 F:718-809/Region: repeat
 F:727-726/Region: repeat
 F:727-735/Region: repeat
 F:736-744/Region: repeat
 F:745-753/Region: repeat
 F:754-762/Region: repeat
 F:763-771/Region: repeat
 F:772-780/Region: repeat
 F:781-789/Region: repeat
 F:792-800/Region: repeat
 F:801-809/Region: repeat
 F:556/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 63.6%; Score 49; DB 1; Length 955;
 Best Local Similarity 58.3%; Pred. No. 4;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDIRHSGEGDDL 13
 ||: ||: ||: ||:
 Db 776 NDLHGGKGGDI 787

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RESULT 12
139643
RTX-toxin I - Actinobacillus pleuropneumoniae
N:Alternate names: hemolysin Apxi
C:Species: Actinobacillus pleuropneumoniae
C>Date: 19-Jul-1996 #sequence-revision 08-Nov-1996 #text-change 18-Jun-1999
C:Accession: I39643; S18769; I39645; S60732; S35781
R:Jansen, R.; Bittaire, J.; Kamp, E.M.; Gielkens, A.L.; Smits, M.A.
J Infect. Immun. 61, 3688-3695, 1993
A:Title: Structural analysis of the Actinobacillus pleuropneumoniae-RTX-toxin I (Apxi)
A:Reference number: I39641; MUID:93366425
A:Accession: I39643
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-1022 <RES>
A:Cross-references: EMBL:X73117; NID:g312897; PIDD:CAA51548.1; PID:g312899
R:Prey, J.; Meier, R.; Gygis, D.; Nicolet, J.
Infect. Immun. 59, 3026-3032, 1991
A:Title: Nucleotide sequence of the hemolysin I gene from Actinobacillus pleuropneumoniae
A:Reference number: S18769; MUID:91348845
A:Accession: S18769
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-209, 'AMPYLTAA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <PRE>
A:Cross-references: EMBL:X52899; NID:g38949; PIDD:CAA37081.1; PID:g38950
R:Prey, J.; Halldmann, A.; Nicolet, J.; Boffin, A.; Prenzki, P.
Gene 142, 97-102, 1994
A:Title: Sequence analysis and transcription of the apxi operon (hemolysin I) from Actinobacillus pleuropneumoniae
A:Reference number: I39644; MUID:94237497
A:Accession: I39645
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-209, 'AMPYLTAA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <RES>
A:Cross-references: EMBL:X68595; NID:g505568; PIDD:CAA48586.1; PID:g505570
R:Tascon, R.I.; Vazquez-Boland, J.A.; Gutierrez-Martin, C.B.; Rodriguez-Barbosa, I.; Rod
Mol. Microbiol. 14, 207-216, 1994
A:Title: The RTX hemolysins Apxi and ApxiI are major virulence factors of the swine pathogen
A:Reference number: S60731; MUID:95317473
A:Accession: S60732
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 604-685 <TRAS>
A:Comment: This organism causes porcine pleuropneumonia.
C:Genetics:
A:Gene: apxiA
C:Function:
A:Description: attacks blood cell membranes and causes cell lysis
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytotoxins; exotoxins; hemolysis; lipoprotein; tandem repeat;
F:243-789/Domain: hemolysin A homology <HLVA>
F:721-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYF]-X)
F:560,686/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 63.6%; Score 49; DB 1; Length 1022;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFSGEGDD 12
DB 733 FTDIFHGAKGDD 744

RESULT 13
E69361
signal-transducing histidine kinase homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence-revision 05-Dec-1997 #text-change 02-Sep-2000
C:Accession: E69361
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

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Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Overbeek, R.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kalne, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: E69361
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-334 <KLE>
A:Cross-references: GB:AE001042; GB:AE000782; NID:g2689365; PIDD:AAB90347.1; PID:g264
C:Superfamily: sensor histidine kinase homology
F:120-330/Domain: sensor histidine kinase homology <SKH>

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Query Match 62.3%; Score 48; DB 2; Length 334;
Best Local Similarity 69.2%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFSGEGDD 13
DB 285 FNEGFSGEGQL 297

RESULT 14
LESCA
hemolysin A - Escherichia coli
C:Species: Escherichia coli
C>Date: 30-Sep-1988 #sequence-revision 30-Sep-1988 #text-change 18-Jun-1999
C:Accession: A24433; I41280
R:Felmler, T.; Pellet, S.; Welch, R.A.
J. Bacteriol. 163, 94-105, 1985
A:Title: Nucleotide sequence of an Escherichia coli chromosomal hemolysin.
A:Reference number: A24433; MUID:85234404
A:Accession: A24433
A:Molecule type: DNA
A:Residues: 1-1023 <FE>
A:Cross-references: GB:M10133; GB:M12863; NID:g146377; PIDD:AAA23975.1; PID:g146379
R:Stanley, P.; Packman, L.C.; Koronakis, V.; Hughes, C.
Science 266, 1992-1996, 1994
A:Title: Fatty acylation of two internal lysine residues required for the toxic acti
A:Reference number: A55387; MUID:95099325
A:Contents: annotation: lysine palmitoylation
A:Note: lysine modification is performed by the hlyC gene product
R:Haertlein, M.; Schlessel, S.; Wagner, W.; Rdest, U.; Krefel, J.; Goebel, W.
J. Cell Biol. 22, 87-97, 1983
A:Title: Transport of hemolysin by Escherichia coli.
A:Reference number: I41280
A:Accession: I41280
A:Status: translated from GB/EMBL/DDBT
A:Molecule type: DNA
A:Residues: 1, 'T', '3', 'V', '5', 'T', '7-44 <RES>
A:Cross-references: GB:M29173; NID:g146337; PIDD:AAA23957.1; PID:g146338
C:Genetics:
A:Gene: hlyA
C:Function:
A:Description: attacks blood cell membranes and causes cell lysis
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytotoxins; exotoxins; hemolysis; lipoprotein; tandem rep
F:246-791/Domain: hemolysin A homology <HLVA>
F:723-851/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYF]-X)
F:563,689/Binding site: palmitate (lys) (covalent) #status experimental

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Query Match 62.3%; Score 48; DB 1; Length 1023;
Best Local Similarity 66.7%; Pred. No. 6.3;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFSGEGDD 12
DB 735 FADIFHGAGDD 746

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RESULT 15

AD2546
hypothetical protein all17655 [imported] - Anabaena sp. (strain PCC 7120) plasmid pcc7120
C:Species: Anabaena sp.
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AD2546
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, S.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD2546
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-302 <KUR>
A:Cross-references: GB:AP003602; PIDN:BAE7298.1; PID:q17134740; GSPDB:GN00181
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all17655
A:Genome: plasmid

Query Match 61.0%; Score 47; DB 2; Length 302;
Best Local Similarity 75.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 DIFHSGEGDDL 14
||| | |||
DB 85 DIFHRGAGDDL 96

Search completed: September 11, 2002, 09:00:14
Job time: 232 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2002, 08:59:26 : Search time 30.68 Seconds
(without alignments)
11.146 Million cell updates/sec

Title: US-09-884-696-13
Perfect score: 77
Sequence: 1 FNDIFHSGEDDL 14

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	75.3	1049	3	US-08-772-270A-11
2	58	75.3	1244	5	PCT-US93-10500-2
3	52	67.5	758	1	US-08-258-188-2
4	52	67.5	758	1	US-08-526-813-2
5	52	67.5	758	5	PCT-US95-08554-2
6	49	63.6	924	3	US-08-619-812-8
7	49	63.6	926	1	US-07-908-253-2
8	49	63.6	926	1	US-08-455-970A-2
9	49	63.6	926	1	US-08-387-156-6
10	49	63.6	926	2	US-08-694-865-6
11	49	63.6	926	2	US-08-878-748-6
12	49	63.6	926	2	US-08-535-837-2
13	49	63.6	926	3	US-09-124-491-6
14	49	63.6	926	6	5476657-3
15	49	63.6	936	1	US-08-455-970A-12
16	49	63.6	943	1	US-08-455-970A-10
17	49	63.6	951	1	US-08-455-970A-14
18	49	63.6	977	1	US-08-387-156-8
19	49	63.6	977	2	US-08-694-865-8
20	49	63.6	977	2	US-08-878-748-8
21	49	63.6	977	3	US-09-124-491-8
22	49	63.6	1022	3	US-08-772-270A-2
23	49	63.6	1069	1	US-07-777-715-9
24	49	63.6	1069	1	US-08-170-126-4
25	49	63.6	1069	3	US-08-954-418-4
26	49	63.6	1098	1	US-07-777-715-7
27	49	63.6	1098	1	US-08-170-126-2

28	49	63.6	1098	3	US-08-954-418-2	Sequence 2, Appl
29	46	59.7	956	3	US-08-772-270A-8	Sequence 8, Appl
30	45	58.4	934	1	US-08-215-805A-80.	Sequence 80, Appl
31	42	54.5	1706	4	US-08-669-785-2	Sequence 2, Appl
32	42	54.5	1794	6	5183745-6	Sequence 43, Appl
33	41	53.2	153	2	US-08-387-942C-43	Sequence 4, Appl
34	41	53.2	1403	2	US-08-387-942C-3	Sequence 3, Appl
35	41	53.2	1705	4	US-08-669-785-4	Sequence 4, Appl
36	40	51.9	213	1	US-09-609-324A-10	Sequence 10, Appl
37	40	51.9	213	2	US-08-920-440B-10	Sequence 10, Appl
38	40	51.9	213	4	US-09-173-492-10	Sequence 10, Appl
39	40	51.9	213	4	US-09-173-133-10	Sequence 10, Appl
40	40	51.9	823	1	US-07-745-206A-15	Sequence 15, Appl
41	40	51.9	823	2	US-08-311-363-15	Sequence 15, Appl
42	40	51.9	1754	1	US-07-745-206A-13	Sequence 13, Appl
43	40	51.9	1754	2	US-08-311-363-13	Sequence 13, Appl
44	40	51.9	2237	1	US-08-455-943A-48	Sequence 48, Appl
45	40	51.9	2237	2	US-08-223-305C-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-08-772-270A-11
: Sequence 11, Application US/08772270A
: Patent No. 6019984
: GENERAL INFORMATION:
: APPLICANT: MacInnes, Janet
: APPLICANT: Ricciardi, Paul
: APPLICANT: Mallard, Bonnie
: APPLICANT: Rosendal, Soren
: TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESSES:
: STREET: 40 King Street West
: CITY: Toronto
: STATE: Ontario
: COUNTRY: Canada
: ZIP: M5H 3Y2
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/772,270A
: FILING DATE: December 23, 1996
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Gravelle, Michelle
: REGISTRATION NUMBER: 40,261
: REFERENCE/DOCKET NUMBER: 6580-81
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (416) 364-7311
: TELEFAX: (416) 361-1398
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1049 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: ORIGINAL SOURCE:
: ORGANISM: Actinobacillus pleuropneumoniae
: US-08-772-270A-11

Query Match 75.3%; Score 58; DB 3; Length 1049;
Best Local Similarity 71.4%; Pred. No. 0.11;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEGDDL 14
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Db 747 FNDIFHSGADGDDL 760

RESULT 2
PCT-US93-10500-2
: Sequence 2, Application PC/TUS9310500
: GENERAL INFORMATION:
: APPLICANT: Chang, Yung-Fu
: TITLE OF INVENTION: Recombinant Vaccine For Procine
: PLEUROPNEUMONIAE
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Alan S. Korman
: STREET: 1600 Empire Tower
: CITY: Buffalo
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 14202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/10500
: FILING DATE:
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/972,229
: FILING DATE: 05-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Korman, Alan S.
: REGISTRATION NUMBER: 33,932
: REFERENCE/DOCKET NUMBER: 19603/00001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 716-853-8104
: TELEFAX: 716-853-8109
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1244 amino acids
: TYPE: amino acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: ORIGINAL SOURCE:
: ORGANISM: Actinobacillus pleuropneumoniae
: STRAIN: Serotypes 2, 3, 4, 6 and 8
: INDIVIDUAL ISOLATE: Swine
: CELL TYPE: Gram negative bacterium
: PCT-US93-10500-2

Query Match 75.3%; Score 58; DB 5; Length 1244;
Best Local Similarity 71.4%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEGDDL 14
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Db 920 FNDIFHSGADGDDL 933

RESULT 3
US-08-258-188-2
: Sequence 2, Application US/08258188
: Patent No. 5475098
: GENERAL INFORMATION:
: APPLICANT: Hall, Robert H.

APPLICANT: Xu, Jian Guo
: TITLE OF INVENTION: A NEW AND DISTINCTIVE DNA SEQUENCE OF E.
: COLI O157:H7 AND ITS USE FOR THE RAPID, SENSITIVE AND
: SPECIFIC DETECTION OF O157:H7 AND OTHER ENTEROHEMORRHAGIC
: E. COLI
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: Steuart Street Tower, One Market Plaza
: CITY: San Francisco
: STATE: California
: COUNTRY: US
: ZIP: 94105-1493
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/258,188
: FILING DATE: 14-JUN-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Garrett-Mackowski, Eugenia
: REGISTRATION NUMBER: 37,330
: REFERENCE/DOCKET NUMBER: 15280206, DHHS135940
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 543-9600
: TELEFAX: (415) 543-5043
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 758 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-258-188-2

Query-Match 67.5%; Score 52; DB 1; Length 758;
Best Local Similarity 57.1%; Pred. No. 0.75;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEGDDL 14
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Db 480 FNDIFHSGADGNDYI 493

RESULT 4
US-08-526-813-2
: Sequence 2, Application US/08526813
: Patent No. 5756293
: GENERAL INFORMATION:
: APPLICANT: Hall, Robert H.
: APPLICANT: Xu, Jian Guo
: TITLE OF INVENTION: A New and Distinctive DNA Sequence of E.
: COLI O157:H7 and its Use for the Rapid, Sensitive and
: SPECIFIC DETECTION OF O157:H7 and Other Enterohemorrhagic
: E. COLI
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/526,813
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,188
FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-206-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-526-813-2

Query Match 67.5%; Score 52; DB 1; Length 758;
Best Local Similarity 57.1%; Pred. No. 0.75;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNDIFHSGEDDL 14
||||| :| :
Db 480 FNDIFHGADGNDYI 493

RESULT 5
PCT-US95-08554-2
Sequence 2, Application PC/TUS9508554
GENERAL INFORMATION:
APPLICANT: HALL, Robert H.
APPLICANT: XU, Jian Guo
TITLE OF INVENTION: A NEW AND DISTINCTIVE DNA SEQUENCE OF E.
TITLE OF INVENTION: COIL 0157:H7 AND ITS USE FOR THE RAPID, SENSITIVE AND
TITLE OF INVENTION: SPECIFIC DETECTION OF 0157:H7 AND OTHER ENTEROHEMORRHAGIC
TITLE OF INVENTION: E. coli
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08554
FILING DATE: 14-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280206, DHHSEL35940
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08554-2

Query Match 67.5%; Score 52; DB 5; Length 758;
Best Local Similarity 57.1%; Pred. No. 0.75;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNDIFHSGEDDL 14
||||| :| :
Db 480 FNDIFHGADGNDYI 493

RESULT 6
US-08-619-812-8
Sequence 8, Application US/08619812
Patent No. 6100066
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: THEISEN, MICHAEL
APPLICANT: HARLAND, RICHARD J.
APPLICANT: RIOUX, CLEMENT R.
TITLE OF INVENTION: VACCINES FOR HAEMOPHILUS SOMNUS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,812
FILING DATE: 15-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/038,719
FILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0019.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-619-812-8

Query Match 63.6%; Score 49; DB 3; Length 924;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEDDL 13
||| :| :
Db 747 NDILHSGGDDI 758

RESULT 7
US-07-908-253-2
Sequence 2, Application US/07908253
Patent No. 5534256
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE

TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,253
FILING DATE: 19920702
CLASSIFICATION: 420
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-908-253-2

Query Match 63.6%; Score 49; DB 1; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13
||:|:|:|:
Db 747 NDHLHGKGD1 758

RESULT 8
US-08-455-970A-2
Sequence 2, Application US/08455970A
Patent No. 5708155
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HOW P. A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
TITLE OF INVENTION: CHIMERAS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,970A
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992

ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-455-970A-2

Query Match 63.6%; Score 49; DB 1; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13
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Db 747 NDHLHGKGD1 758

RESULT 9
US-08-387-156-6
Sequence 6, Application US/08387156
Patent No. 5723129
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HOW P. A.
TITLE OF INVENTION: GHR-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-387-156-6

Query Match 63.6%; Score 49; DB 1; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13
||:|:|:|:
Db 747 NDILHGKGD1 758

RESULT 10

US-08-694-865-6
; Sequence 6, Application US/08694865
; Patent No. 5837268
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: MANN, JOHN G.
; TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS LLP
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/694,865
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 9001-0016.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)327-3400
; TELEFAX: (415)327-3231
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-694-865-6

Query Match 63.6%; Score 49; DB 2; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13
||:|:|:|:
Db 747 NDILHGKGD1 758

RESULT 11

US-08-878-748-6
; Sequence 6, Application US/08878748
; Patent No. 5969126
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HOW P. A.
; TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO

STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,748

FILING DATE: 19-JUN-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,156

FILING DATE: 10-FEB-1995

APPLICATION NUMBER: US 07/960,932

FILING DATE: 14-OCT-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171

FILING DATE: 16-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016.21

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-878-748-6

Query Match 63.6%; Score 49; DB 2; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13
||:|:|:|:
Db 747 NDILHGKGD1 758

RESULT 12

US-08-535-837-2
; Sequence 2, Application US/08535837
; Patent No. 5985289
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: HARLAND, RICHARD J.
; TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBERTA L. ROBINS
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,837
; FILING DATE: 27-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0026.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-535-837-2

Query Match 63.6%; Score 49; DB 2; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13
||: ||: ||:
Db 747 NDHLHGKGD1 758

RESULT 13
US-09-124-491-6
Sequence 6, Application US/09124491
Patent No. 6022960

GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,491
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/694,865
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-491-6

Query Match 63.6%; Score 49; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13
||: ||: ||:
Db 747 NDHLHGKGD1 758

RESULT 14

5476657-3

PATENT NO. 5476657
APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: PASTEURIZED HEMOLYTIC LEUKOTOXIN
COMPOSITIONS AND USES THEREOF
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/15,537
FILING DATE: 09-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,850
FILING DATE: 05-APR-1990
APPLICATION NUMBER: 335,018
FILING DATE: 07-APR-1989
SEQ ID NO: 3:
LENGTH: 926

5476657-3

Query Match 63.6%; Score 49; DB 6; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13
||: ||: ||:
Db 747 NDHLHGKGD1 758

RESULT 15

US-08-455-970A-12

Sequence 12, Application US/08455970A
Patent No. 5708155

GENERAL INFORMATION:

APPLICANT: POTTER, ANDREW A.

APPLICANT: REDMOND, MARK J.

TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS

STREET: 285 HAMILTON AVENUE, SUITE 200

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,970A

FILING DATE: 31-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/960,932

FILING DATE: 14-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 936 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-455-970A-12

Query Match 63.6%; Score 49; DB 1; Length 936;
Best Local Similarity 58.3%; Pred. NO. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 NDIFHSGGDDL 13
II: I:III:
Db 747 NDILHGKGDDI 758

Search completed: September 11, 2002, 08:59:26
Job time: 209 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:57:17 ; Search time 22.74 Seconds

(without alignments)
1578.409 Million cell updates/sec

Title: US-09-884-696-2

Sequence: 1 MSNINVIKSNINQAGLNSTKS.....SSNALPIPTPTOSTLAPSV 927

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2334	50.2	953	LKAL_PASHA	P16535 Pasteurella
2	2332	50.2	953	LKAB_PASHA	P55135 Pasteurella
3	2310	49.7	947	LKTA_PASSP	P55123 Pasteurella
4	2256	48.6	953	LKTA_PASHA	P55116 Pasteurella
5	2240.5	48.2	956	RTA2_ACTPL	P15377 actinobacill
6	2236	48.1	955	LKAA_PASHA	P55117 Pasteurella
7	2218.5	47.8	956	HLVA_ACTSU	Q00951 actinobacill
8	1959.5	42.2	1052	RT32_ACTPL	P55130 actinobacill
9	1928	41.5	1049	RT31_ACTPL	P08715 escherichia
10	1852.5	39.9	1024	HLVA_ECOLI	P09883 escherichia
11	1849	39.8	1023	HLV1_ECOLI	P55129 escherichia
12	1733.5	37.3	1023	RT12_ACTPL	P55128 actinobacill
13	1727	37.2	1023	RT11_ACTPL	P16462 actinobacill
14	1716.5	36.9	1050	LKTA_ACTAC	P15318 bordetella
15	806	17.3	1706	CYAA_BORPE	P55127 neisseria
16	805.5	17.3	1705	CYAA_BORPE	P55127 neisseria
17	434	9.3	1829	FRPC_MEIMC	Q919V5 neisseria m
18	432.5	9.3	1829	FRPC_MEIMB	Q919V5 neisseria m
19	416	9.0	1302	FRPA_NEIMB	P55126 neisseria m
20	403.5	8.7	1115	FRPA_NEIMC	P55126 neisseria m
21	190.5	4.1	1608	HLVA_SERMA	P15320 serratia ma
22	188.5	4.1	2869	RBP1_PLAVB	Q00798 plasmodium
23	183.5	3.9	1577	HLVA_PROMI	P16466 proteus mir
24	178.5	3.8	284	NODO_RHIV	P15728 rhizobium l
25	175.5	3.7	1228	SLAP_BACST	P35828 bacillus st
26	173.5	3.7	1520	SLAP_CAUCR	O991b0 caulobacter
27	173	3.7	1520	RMPD_CHIMU	O991b0 chlamydia m
28	171	3.7	1251	RBP2_PLAVB	Q00799 plasmodium
29	171	3.7	1656	OMPB_RICUA	Q06653 r outer mem
30	171	3.7	2249	OMPA_RICRI	P15137 rickettsia
31	170	3.7	491	ZAPA_PROMI	Q11137 proteus mir
32	165.5	3.6	1592	GTF2_STRDO	P27470 streptococc
33	165	3.6	479	PRTC_ERWCH	P16317 erwania chr

ALIGNMENTS

RESULT	ID	STANDARD	PRT	953 AA
1	LKAL_PASHA			
AC	P16535			
DT	01-AUG-1990 (rel. 15, Created)			
DT	01-AUG-1990 (rel. 15, Last sequence update)			
DT	30-MAY-2000 (rel. 39, Last annotation update)			
DE	Leukotoxin from serotype A1.			
GN	LKTA			
OS	Pasteurella haemolytica.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;			
OC	Mannheimia.			
OX	NCBI_TaxID=75985;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN-SEROTYPE A1:			
RX	MEDLINE=87306837; PubMed=3040588;			
RA	Lo R.Y.C., Strathdee C.A., Shewen P.E.;			
RT	"Nucleotide sequence of the leukotoxin genes of Pasteurella			
RT	haemolytica A1."			
RL	Infect. Immun. 55:1987-1996(1987).			
RN	[2]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN-SEROTYPE A1 / PHL101;			
RX	MEDLINE=89210283; PubMed=2707120;			
RA	Higlander S.K., Chidambaram M., Engler M.J., Weinstein G.M.;			
RT	"DNA sequence of the Pasteurella haemolytica leukotoxin gene			
RT	cluster."			
RL	DNA 8:15-28(1989).			
RN	[3]			
RC	SEQUENCE OF 884-953 FROM N.A.			
RC	STRAIN-SEROTYPE A1 / PHL101;			
RX	MEDLINE=90236888; PubMed=2185213;			
RA	Higlander S.K., Engler M.J., Weinstein G.M.;			
RT	"Secretion and expression of the Pasteurella haemolytica leukotoxin."			
RT	J. Bacteriol. 172:2343-2350(1990).			
CC	- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD			
CC	CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY			
CC	DEFINED.			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING			
CC	CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC			
CC	ACTIVITY.			
CC	- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE			
CC	INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).			
CC	- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN			
CC	MODIFIED (BY SIMILARITY).			
CC	- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.			
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			

34	164.5	3.5	475	1	PRTC_ERWCH	007162 erwania chr
35	164.5	3.5	1609	1	PM21_CHLPP	O926U5 chlamydia p
36	164	3.5	1250	1	YFAL_ECOLI	P45508 escherichia p
37	163	3.5	918	1	YMOB_CAEEL	P34487 caenorhabd1
38	163	3.5	1713	1	YDAA_HUMAN	Q16787 homo sapien
39	162.5	3.5	2003	1	YDAA_ECOLI	P33666 escherichia
40	161	3.5	2366	1	TOXB_CLODI	P18177 clostridium
41	159.5	3.4	487	1	PRZN_SERMA	P23694 serratia ma
42	159	3.4	1569	1	YFUA_ECOLI	P52143 escherichia
43	157	3.4	1655	1	OMPB_RICCN	Q9KRA3 r outer mem
44	156.5	3.4	933	1	SLAP_CAMEE	P35827 campylobact
45	156.5	3.4	3712	1	LMA_DROME	Q00174 drosophila

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CC -----
DR EMBL: M20730; AAA25529.1; -
DR EMBL: M24197; AAA25343.1; -
DR PIR: S29516; S29516.
DR HSSP: P02392; ICTF.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RTX_A.
DR Pfam: PF00353; hemolysincabind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABINDGRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4.
KW Hemolysis: Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
  Transmembrane; Lipoprotein; Palmitate.
FT TRANSMEM 229 249 POTENTIAL.
FT TRANSMEM 297 318 POTENTIAL.
FT TRANSMEM 366 390 POTENTIAL.
FT DOMAIN 734 784 6 X REPEATS, GLY-RICH (BY SIMILARITY).
FT REPEAT 734 739 1.
FT REPEAT 743 748 2.
FT REPEAT 752 757 3.
FT REPEAT 761 766 4.
FT REPEAT 770 775 5.
FT REPEAT 779 784 6.
FT REPEAT 409 414 FEHYAN -> LSTLOI (IN REF. 2).
FT CONFLICT 742 742 D -> Y (IN REF. 2).
FT SEQUENCE 953 AA; 101996 MW; 7F93D113A118C05F CRC64;

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Query Match 50.2%; Score 2334; DB 1; Length 953;
Best Local Similarity 50.1%; Pred. No. 1,le-112;
Matches 465; Conservative 175; Mismatches 263; Indels 26; Gaps 13;

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QY 8 KSNQAGINSTKSGKLNXYLAIPKD--YDPKGGTINDFTKADELGAARAEENHET 65
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DB QSLTVQAG-SSLKTGAKKILTYIPQYQYDTGQGLDVLVAAELRLEGEVREERNKNT 86
QY 66 AKKSVDTVNOFLSTLOTGIAISATKLEKFLQKHSNKLAKGLDSVENIDRKLGKASVLS 125
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB AOTSIGTGTOTATGILFERIVLSPQIDKLLK---TKGQALGSAGESLYQANNAKATVLS 143
QY 126 TLSSFLGALAGIELDLSITKGGDAAPDLAKASIDLINETIGNLSQSQTTEAFSSQLAK 185
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB GIQSITLGSVLGMDLEAL-QNNSQHALAKAGELTSLLENTIANSVKTTDEFEQOISQ 202
QY 166 LGSTISQAKGFSNIGNKQNL-NFSKTMIGLEITIGLSISAGPALDKNASTKKYVA 244
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB FGSKLQNIKGLGTLGDKLKNIGLDKAGLDVIGSLSGATPAVLADKNASTAKKYGVA 262
QY 203 FGSKLQNIKGLGTLGDKLKNIGLDKAGLDVIGSLSGATPAVLADKNASTAKKYGVA 262
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 245 GFELSNQVIGNVTKAISSYVLAQRYAAGLSTTGAVAAALITSSIMLAISPLAFMNAADKN 304
DB :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB GFELANQVIGNVTKAVSSYVLAQRYAAGLSTTGAVAAALITSSIMLAISPLAFMNAADKN 322
QY 305 HANALDEFAKQRFKFGYGGDHLAAYGQGVTEIETSLTTISALGAVSAGSAAVGSNAV 364
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB HAKSLSEYAERKKLGYGNDLAEYQGTGTIDASVTAINTALAIAGVSAAAGSVYI 382
QY 365 GAPIVLAVAGYGLSIGLIEASQAMFESVANRLQGLKLEWKGONGONYEPDGYSRYA 424
DB :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB ASPILLVSGITGVSTILQYSKQAMFEVANKINKIKYEMKNHGNKYPENGDAYRL 442
QY 425 AYLANNLKFSELNLEAEVRYAIAITQQRWNNIGELAGITKLGRIKSGAYADAFEDG 484
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB ANLQNNMFKFLNLNKELEAEVRYAIAITQQRWNNIGELAGISRLGKRVLSGKAYVAFEEG 502
QY 443 KKEVGSNTLDAKTGIIDISNSNGKKTQALHFTSPLTAGESBRLNKGYSYINKLK 544
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 503 KHIXADKLVQDLDSANGIIDVNSNGRAKQIHLFRPLPLPGTHERREVQGTGYEYITKLN 562
QY 545 FGRVNMQVTDGEASKGLDFSKVIQV-----AETEGTDIGLIVAKAANDDIQVGO 597
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 563 INKVDSWKITTDGAASSTFDLINVQRIEGLDNDAGNVKTRKTKTIIAKLGEDDANVFVS 622

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QY 598 GKNNIDGDCGDRVYFSKDGFCNITVDGTSATEAGSYTVNRKVARGDYIHEVYKQETK 657
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DB 623 GTTEIDGGEYDVKYHSR-GNYCALITIDATKEFGQSYTVNRVVEYKALHETSHNTAL 681
QY 658 VGRKRTETIQRDYELRKVGYGOSTNLASVEEVISQFNDVFKSGFNDIHSGGDDI 717
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 682 VGNREEKIEYR-HSNQHNHAGYTYTKDLKAVEEIIETSHNDIFKSGKPFDAFNGGCVDT 740
QY 718 LDDGAGDDRLFGGKGNDRSLGSGDDDLDDGGSDDVYUNGAGNDVYIFRKGDDNDTLVYG 777
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 741 IDGNDGNDRLFGKAGDDILDGNGDDPFDGKGNDLHGKGDIVYHRKGDDNDITLTS 800
QY 778 TGNDKLAFAFADANISDIMEETKEGIIYKRNDSGSINIPRWY---TTSNLQNYQSNKTD 833
DB :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 801 DGNDKLSFSDSNLKDILFEKVKHNLVI-TNSKKEKVTIQWVFREADFAKVPYKATK-D 858
QY 834 HKIEQLIGKGSYITSQIDKILQDKDQVITISOELKRLADENKSGKLSASDIASLKN 893
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 859 EKIEEIIIGONGERTTSKQVDDL-AKGNCKITQDELISKVVDVYELKHS-KNVTISLDR 915
QY 894 LVGSMALFGTANSVSSNALQPTOPTQGI 922
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 916 LISSVAFSSNDGRNVLVAPTSMLDQSL 944

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RESULT 2
LKAB_PASHA STANDARD; PRT; 953 AA.
ID LKAB_PASHA
AC P55118:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Leukotoxin from serotype A11.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OC NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SEROTYPE A11; PubMed=8225575;
RX MEDLINE=94041617;
RA Burrows L.L., Olah Winfield F., Lo R.Y.C.;
RT "Molecular analysis of the leukotoxin determinants from Pasteurella
  haemolytica serotypes 1 to 16."
RL Infect. Immun. 61:5001-5007(1993).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
  CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
  DEFINED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
  CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
  ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
  INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PFM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
  MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARIOTIC TOXIN FAMILY.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U01215; AAB36689.1; -
CC InterPro: IPR001343; Hemlysn_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC InterPro: IPR003995; RTX_A.
CC Pfam: PF00353; hemolysincabind; 1.

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FT REPEAT 739 744 3.
 FT REPEAT 748 753 4.
 FT REPEAT 757 762 5.
 FT REPEAT 766 771 6.
 FT REPEAT 775 780 7.
 SQ SEQUENCE 947 AA; 101559 MW; 9744F06395FE5BED CRC64;

Query Match 49.7%; Score 2310; DB 1; Length 947;
 Best Local Similarity 50.1%; Pred. No. 1.8e-111;
 Matches 467; Conservative 173; Mismatches 252; Indels 40; Gaps 16;

1 MSNIN-1KSNIOAGINST-----KSGIKNLYAIAPKD--YDPOKGTLLNDEIK 46
 4 LANISTNKNLSQSLHNTGSLNAGSLKAGAKKLLIYIPKDYSGRNGSLDLYK 63
 47 AADELGIRLAEPPNHTAKKSVTVNOFLSTOTGIAISATKIEKLOKHSHTKLAKG 106
 64 AAEDGIEVOREERNGIATAONSLETONIIGFSEKGVLPAPOLDKLOK--KISKA 120
 107 LDSVENIDRKLGKASNVSTLSSFLGTALAGIELDSLKKGDAPDALAKASIDLINELI 166
 121 PSSSENVAKNLGNMOTLLSGISITIGSVAMGMDDEILKNGSELD-LAKAGLELTNLI 179
 167 GNLSTOTIEAFSSQIAKLGSTISQAKFNSNGKLN-ESKTNLGLLEITIGLSGI 225
 180 ENIANSVOTLDTFSEQISOLGFKLQNVKGLGTLDKLNKFSGSKAGLGLVIGLSGA 239
 226 SAGFALADKNATGKKVAAGFELSNOVIGNVTKAISVYLORVAAGISTGAVALLTS 285
 240 TAAVLADKNASTDRKVGAFELANOVGNITKAVSYILORVAAAGLSTNGVSALLAS 299
 286 STMLAISPLAFNMAADKFNHANALDEFAKQFRFGYDGDHLLAEYORGVTEASTLTS 345
 300 TAAIAISPLAFAGIADKFNNAKALSYAEKFKLGEGLSLAEYORGVTEASTAVN 359
 346 TALGAVSAGVAAVAGSAGAPIALIVAGVGLISGLEASQAMFESVANKLQKILEM 405
 360 TALAIAISGVSAAGSLGAPIALIVSGITISITLQYKSAEHNANKHKKIDW 419
 406 EKONGONFEDKGYDSRYAAYLANNLKFLSENLKELEARVAITQORMDNNGELAGIT 465
 420 EKKHNGKNTFENGYSRYIADIDQNMROJONLKELOARVIRITQOQMDNNGELAGIS 479
 466 KLGERIKSKAYADAFFEDKQVAGSNTLLDAKGTIIDISNSNGKQALHFTSPLLTAG 525
 480 RIGEKVMSKAYADAFFEEKLIKADTFVOLDATGVIYNTSKSDNYKTOHILERTPLAPG 539
 526 TESRELTNGKTSYINKLKFGRYKMOVYDGAASSKLDPSKYIQRA-----ETEGTD 578
 540 VERRERIQTKYEYITIKLININRYDSWKITDGNSTFEDLTNNVIRIGIELDHADVTKY 599
 579 EGLIYNAKAGNDIPVGGKKNIDGGDHDHRYFYSKDGSGFNITVDTGSAEAGSYTN 638
 600 ERTIANDLDGNDVFTIGCTTEVDGNGLDHYHR-GDYCALITIDATNESVQSGYTK 658
 639 RKVARGDIYHEVVKROETVYKRTETIQRDYELRKRVGYGYSTDNLKSVEEYISQFND 698
 659 RFVETKALHEVYATQSVLVGSSEKIEYR-HSNNTQHGAYTTDPLKVEELIGHSRND 717
 699 VRKGSFNDIFHSGBEDDLIDGAGDRLFGKGNRLSGDEBDDLIDGSGDDVYNGA 758
 718 IFKGSFDDAFHGGDGDVNDIDGAGNDRLFGGKGFIDIDCGDDDFIDGSGDDILHGG 777
 759 GNVYIFRKGDDGNDLYDGGNDKLAFAADANISDIIEFRKEGIYKRDHSGSINIPW 818
 778 GNDILCTVAG-GNDSISDSGNDRLSFADSNLKDILFEKYNHMLT-TVKKKEKVIQW 835
 819 Y---TTSNLQYQSNKTDHRTBOLIGKDGSYTSDQIDKILQDKRGVITVTSQELKLA 874
 836 FREADYAKTVHNYQAT-ADEKIEIIGRGERITSKQIDELIEKGG--KIDSELERIA 892
 875 DENKSOKLASDIAS-SLNKLVSMLFGTAN 905

Db 893 E--SSALLKESKFSASNSLNKLVSAGAFASN 922

RESULT 4
 ID LKA3_PASHA STANDARD; PRT; 953 AA.
 AC P5116;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Leukotoxin from serotype T3.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SEROTYPE T3;
 RX MEDLINE=94041617; PubMed=8225575;
 RA Burrows L.L., Lo R.Y.C., Olah-Winfield E.;
 RT "Molecular analysis of the leukotoxin determinants from Pasteurella
 haemolytica serotypes 1 to 16".
 RL Infect. Immun. 61:5001-5007(1993).
 CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
 CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
 CC DEFINED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 CC ACTIVITY.
 CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
 CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 CC MODIFIED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
 CC
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 CC
 CC EMBL: U01216; AAB36691.1; -.
 CC HSSP: P02392; ICTP.
 CC InterPro: IPR001343; Hemlysn_Ca_bind.
 CC InterPro: IPR003355; RTX_N.
 CC InterPro: IPR003995; RCKA.
 CC Pfam: PF00353; hemolysinCbind; 1.
 CC Pfam: PF02382; RTX; 1.
 CC PRINTS: PR00313; CABNDXNGPT.
 CC PRINTS: PR01488; RTXTOXINA.
 CC PROSITE: PS00330; HEMOLYSIN_CALCIUM; 2.
 CC
 CC HemoIyis: toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
 CC Transmembrane; Lipoprotein; Palmitate.
 CC TRANSMEM 229 249
 CC TRANSMEM 297 318
 CC TRANSMEM 381 401
 CC TRANSMEM 734 784
 CC DOMAIN 734 739
 CC REPEAT 734 739
 CC REPEAT 743 748
 CC REPEAT 752 757
 CC REPEAT 761 766
 CC REPEAT 770 775
 CC REPEAT 779 784
 CC SEQUENCE 953 AA; 101948 MW; FDBDCE2FDC85FDF2 CRC64;

Query Match 48.6%; Score 2256; DB 1; Length 953;
 Best Local Similarity 48.7%; Pred. No. 1.1e-108;

DT	30-MAY-2000	(Rel. 39, Last annotation update)
DE	RTX-II toxin determinant A (APX-IIA) (HLX-IIA)	
DE	(Cytolysin IIA) (CLY-IIA).	
GN	APXIIA OR CLYIIA OR HLXIIA OR APPA OR CYTC.	
OS	Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).	
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;	
OC	Actinobacillus.	
OX	NCBI_TaxID=715;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=SEROTYPE 5;	
RX	MEDLINE=90126233; Pubmed=2693022;	
RA	Cheng Y.-F., Young R., Struck D.K.;	
RT	"Cloning and characterization of a hemolysin gene from Actinobacillus	
RL	(haemophilus) pleuropneumoniae.";	
RN	DNA 8:635-647(1989).	
RP	[2]	
RC	SEQUENCE FROM N.A.	
RC	STRAIN=ISOLATE CVI 13261 / SEROTYPE 9;	
RX	MEDLINE=92040145; Pubmed=1937809;	
RA	Smits M.A., Briatore J., Jansen R., Smith H.E., Kamp E.M.,	
RT	Gielkens A.L.;	
RL	"Cytolysins of Actinobacillus pleuropneumoniae serotype 9.";	
CC	Infect. Immun. 59:4497-4504(1991).	
CC	-1- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.PLEUROPNEUMONIAE,	
CC	WHICH SHOWS A WEAK HEMOLYTIC ACTIVITY AND IS MODERATELY CYTOTOXIC	
CC	FOR ALVEOLAR MACROPHAGES AND NEUTROPHILS.	
CC	-1- SUBCELLULAR LOCATION: Secreted.	
CC	-1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING	
CC	CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC	
CC	ACTIVITY (BY SIMILARITY).	
CC	-1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE	
CC	INVOLVED IN PORE FORMATION BY APXIIIC. THE CYTOTOXIN (BY SIMILARITY).	
CC	-1- PFM: PALMITOYLATED BY APXIIIC. THE TOXIN ONLY BECOMES ACTIVE WHEN	
CC	MODIFIED (BY SIMILARITY).	
CC	-1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.	
CC	-----	
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CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; M30602; AAA87232.1; -;	
DR	EMBL; X61111; CAA43423.1; -;	
DR	PIR; B33389; B33389.	
DR	PIR; S18853; S18853.	
DR	InterPro: IPR001343; Hemlysn_Ca_bind.	
DR	InterPro: IPR003355; RTX_N.	
DR	InterPro: IPR003995; RTX_N.	
DR	Pfam; PF00353; hemolysinCbind; 1.	
DR	Pfam; PF02382; RTX_1.	
DR	PRINTS; PR00313; CAMDNGRPF.	
DR	PRINTS; PR01488; RTXTOXINA.	
DR	PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 1.	
KW	Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;	
KW	Transmembrane; Lipoprotein; Palmitate.	
FT	TRANSMEM 233 256	POTENTIAL.
FT	TRANSMEM 266 323	POTENTIAL.
FT	TRANSMEM 361 406	POTENTIAL.
FT	DOMAIN 719 787	8 X REPEATS, GLY-RICH.
FT	REPEAT 719 724	1.
FT	REPEAT 728 733	2.
FT	REPEAT 737 742	3.
FT	REPEAT 746 751	4.
FT	REPEAT 755 760	5.
FT	REPEAT 764 769	6.
FT	REPEAT 773 778	7.
FT	REPEAT 782 787	8.
SO	SEQUENCE 956 AA; 102531 MW; BDBCABBADF14A641 CRC64;	

Query Match 48.2%; Score 2240.5; DB 1; Length 956;
 Best Local Similarity 47.8%; Pred. No. 7e-108;
 Matches 454; Conservative 188; Mismatches 254; Indels 53; Gaps 15;

QY 1 MSNNV--IKSNIAQGL-----NSTKGLNLYLAIRKDPDQ 36
 DB 1 MSKTTLSLKSSLOOGLKNGKKNLNQACTLLKNGTGTGSHLONAKKLLIYIPQGYDSG 60
 QY KCGTLNDFIKADELIGLARLAEPNHTAKSVDTVNOPLSTOTGIAISATKLEKPLQ 96
 DB 61 QGNVQDLYRKANDLGIEVWREERSNDIAKTSFDTTKILGFDRLGVLFAPOLDNLK 120
 QY KHSNNKLAKGIDSVENIDRKLGKASNVLTSSFLGTALACIELDSLKKDAPDALAK 156
 DB 121 KNP--KIGNTLGSASSISONIGKANTVIGIOSILIGSVLSGVNINELLONNDPNOLEIAK 178
 QY 157 ASIDLINLIIGNLSQOTIEAFSSQALAKGSTISOAKGFNSIGNIKLONL-NFKSTNIGL 215
 DB 179 AGLETLNDELVGNLASSVQTVDAFAQISKLSHLONVGLGSLSKLONLPLDLGKASLGL 238
 QY 216 EITGLISGISAGPALADKNASTGCKKVAAGFELSNOVIGNYTKAISVYLAKQVAAGLST 275
 DB 239 DIISGLISGASAGLILAKKEASTEKKAAGVEFANOIIIGNYTKAVSSYIIAQVASSGLSS 298
 QY 276 TGAVALITSSIMLAISPLAFMAADKFNHANALEDFAKOFRRKGYDGDHLLAEYQGVG 335
 DB 299 TGPVAALIASTVALAVLSPLEFLNADKFKQADLKISYSEKQKIGYDGRLLADFHRETG 358
 QY 336 TIEASLITSTALGAVSGVSAANVGSVAGAPALILVAGVGLISGLIEASKOAMFEVVA 395
 DB 359 TIDSVITINIALAISGCGVAGSGLVAGAPALVAGVGLITLITLIEYSKOAMFEVVA 418
 QY 396 NROGLKILEWKEKONGQNYFPKGYDSRYAAYLANNLKFLSELNKELEAERYAIITQQRWD 455
 DB 419 NKVHDRIYEWKKEH-NKNYFEGGYDSRHLADLDQNMKFLINLKNELQAEVVAITQQQWD 477
 QY 456 NNIGGLAGITLGERIKGKAYADAFFEDGKVEAGSNITTLDAKGTIDISNSKKTAL 515
 DB 478 NOIGGLAISRTDKISSGKAYVAFEEGHOQSYSSVOLNKNKNTINISMTN-RKTOVS 536
 QY 516 HPTSLFAGTESRRLNKGYSYINKLKFQGNWQYTDGASSKLPFSVYIOHVA--- 572
 DB 537 LFRPLILPGEENRRERIEGKNSYITKLIHQRVDSWYITDGDASSVPTNVQRIAYKF 596
 QY 573 -----ETEGTDELGLIVNAKAGNDIIFYOGKMNIDGGCHDRVYFSKDGEGNITVD 625
 DB 597 DDAGNIIESKDTK--IIANLGAGNDVNFVGSSTVIDGQGHDRVHSR-GEYCALYVD 652
 QY 626 GTSATEAGSYVNRKVANGDIYHEVVKROETKVKKRTETIQRYELKAKVGYGSTNUL 685
 DB 653 ATALETGKSYKRYVGDSSKALHETIATHTQNVGNREKIEKR-REDRPFHTGYVTSTSL 711
 QY 686 KSVSEVISOFPNDVFKSGFNDIFHSGEDDLIDGAGDDRLFGGKGNDRISGEGDDL 745
 DB 712 KSVSEIISQFNDIFKSGQFDDVFGNGVDTIDGNDGDHILFGSAGDDVIDGKGNFLL 771
 QY 746 DGGSGDDVINGAGANDVYIFRKGDGNDTLYDGTGNDKLAFADANISIMIERTEKGIIVK 805
 DB 772 VGGTGNDIISGKQNDIYVHKTGNDSDITDGGQDGLAFSDVNLKDLTFKKVDSLEI- 830
 QY 806 RNDHSGSINIPRWY-----ITSMLNVOGSKNTDKHTEQLIGKDGSIITSQDIDKLIQDKD 861
 DB 831 INOKGEKVRIGNMFLEDDIADSTVANYKAT-NDRKIEEITIGKGERITSEYVDKLT--KEG 887
 QY 862 GTVITSQELKRLADENKSGKLSADIASDINKLVGSMALFGANVSSN 910
 DB 888 NNQISAEALSKVYNDYNTSK-DROWNSNSLAKLISVGSFTSSSPFRNN 935

RESULT 6
 LKAA_PASHA STANDARD; PRT: 955 AA.

AC P55117;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Leukotoxin from serotype T10.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SEROTYPE T10;
 RX MEDLINE=96425875; PubMed=8828217;
 RA Lanson F.A., Murray J., Davies R.C., Donachie W.;
 RT "Characterization of epitopes involved in the neutralization of
 RT Pasteurella haemolytica serotype A1 leukotoxin";
 RL Microbiology 142:2499-2507(1996).
 CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
 CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
 CC DEFINED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 CC ACTIVITY.
 CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
 CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 CC MODIFIED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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 CC -----
 DR EMBL; Z26247; CAAB81206.1; -
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR InterPro: IPR003995; RTX_A.
 DR Pfam; PF00353; hemolysincbind; 1.
 DR Pfam; PF02382; RTX; 1.
 DR PRINTS; PR00313; CABNDNGRPT.
 DR PRINTS; PR01488; RTXTOXINA.
 DR PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
 KW Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
 KW Transmembrane; Lipoprotein; Palmitate.
 FT TRANSMEM 299 319 POTENTIAL.
 FT TRANSMEM 361 381 POTENTIAL.
 FT TRANSMEM 383 403 POTENTIAL.
 FT DOMAIN 736 786 6 X REPEATS, GLY-RICH.
 FT REPEAT 736 741 1.
 FT REPEAT 745 750 2.
 FT REPEAT 754 759 3.
 FT REPEAT 763 768 4.
 FT REPEAT 772 777 5.
 FT REPEAT 781 786 6.
 SQ SEQUENCE 955 AA; 102187 MW; B60F2DB8168EBCAF CRC64;

Query Match 48.1%; Score 2236; DB 1; Length 955;
 Best Local Similarity 48.2%; Pred. No. 1.2e-107;
 Matches 458; Conservative 178; Mismatches 271; Indels 44; Gaps 17;
 QY 5 NVKSNIOA---GLN-----STKSGLNLYLAIPND--YDQKGTINDFIKAA 48
 DB 12 NGIRSTLITATRGGLNRACQSLTQAGQYTLKNGAKKILIIYIPDYVYDGGSGGLQDLVKAA 71
 QY 49 DELGATRLAEPNHTETAKKSVDTVNOPLSTOTGIAISATKLEKLOKHSNNKLAKGLD 108

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Db 72 EELGIEVQKEEGNDIAKQAOTSLGTIONVLGTERGIVLSAPOLDKLLK---NKVQALG 128
QY 109 SVENDIRKLGKASNVLTSSSELGFTALAGIELDLSIKKDDAPDALAKSIDLINEITGN 168
Db 129 SSESTAOINESQAKTYVLSVQGSNRIVLACMDIDEAL-QNESDOLTAKAGLEITNSLIN 187
QY 169 LQSOTPTIEAFSSOLAKLTISOAKGFNSIGNKLONL-NFSNTNGLGITLISGISIA 227
Db 188 IANSVOTLDFAFSEQJISQFSKLOANKGALGALGDKLNIGGLDKAGGLGVKSKLLSGATA 247
QY 228 GFALADKNASTGKVAAGFELSNOVIGNVTKAISSVYLAQRYAAGLSTTGAAVALITSSI 287
Db 248 ALVLADKADSTAKKYQACAGELANOVYGNITTKAVSSYLLAQRYAAGLSTTGPAALASTV 307
QY 288 MLASPLAMNAADKFNHNAALDEPAKORRFGYDGDHLLAEQRCVGTESLTTISRA 347
Db 308 AVAISPLSAGIADKFRKAKSLKLENAERPKKLGEGSDSLAEQHTGTIDLSVAINPA 367
QY 348 LGAVSAGVAAVAGSVAVAPIALVAGVTGLISGLEAKSQAMFESVANRLQKILEMER 407
Db 368 LAIAGVSAAGVAAVAPIALVAGVTGLISGLEAKSQAMFESVANRLQKILEMER 427
QY 408 QNGGQNYEDKYDSRYAAYLANNLKFLSELNKELEAERYIAITQORNNIGELAGITKL 467
Db 428 NNGGKRYFENGYDARYLANLQNMKFLNLNKELEAERYIAITQOCMDNIGELAGISRL 487
QY 468 GERIRSGKRYADAFEDGKRYEAGSNTTLAKTCITDINSNKKYQALFTSPLTACTE 527
Db 488 GGRVYLSGKRYAVAFEGQHLKADKVLQDLDSANGIIDVTMTGKQOHLIFRPLPLPTE 547
QY 528 SRERLTNGKRYIYNKLFGRVKNQVTVDEASSKIDFSKVIOVA-----ETEGTDEL 580
Db 548 KREPVOTGKRYEYITKLHTRVDSWQIKDAASSTPDLTVNQRIGVELDHAENVITKET 607
QY 581 GLIYNAKAGNDIIFVGQGMNIDGGDHVRFYSKDGFCNITVDGTSATFAGSYTVNRK 640
Db 608 KIVATLGDSDDMVFWVSGSTTEIDGEGGYDRVHYSR-GNYGALITDATKEFEGSYTVNRF 666
QY 641 VARGDIYHFVVRKQETKVRKRTETIOYRDYELRKVGYGOSTDNKLSVEVIGSQNDVF 700
Db 667 VESGKALHGTSTHTALVNNREKIEYR-HSNNOHHAGYTTKDTLAAVEIITGSHNDIF 725
QY 701 KGSFENDIFHSEGDLDLDGAGDDRLFGKGNDRLSGDEGDDLDLGGSGDDVLLNGAGN 760
Db 726 KGSFENDAFNGGQVDTIDGNGNDRLFGKGGDDIIDGNGDGFIDGKGNLHGGKGD 785
QY 761 DVIYFRKGGNDLTIDGTGNDKLAFADANISDMITERTEGIIYKRNHSGSINIPRWY- 819
Db 786 DIFVHROGGGNDISIESEGNDKLSFSDSNMLKDLTFEKKVNHHLVI-TNTRQEKVTTIONMFR 844
QY 820 ---ITSNLQNYOSNKTDRHIEOLIGDKDSYITSDDOITKILQDKKQDVTYSQELKLADE 876
Db 845 EAEFAKTIONVAYTR-DDKIEIIGONGERITTSKOYDEILE--KGNGKLAQSLELTVVDN 901
QY 877 NKSOKLASDIIASLUNKLVGSMALFETANSVSSNALOPTIPTOGILASV 927
Db 902 YQLAKTS-RDASNSLDKLLSSASAFITSSND-SRNVL---ASPT-SMLDLSL 946

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RESULT 7
HLVA_ACTSU
ID HLVA_ACTSU STANDARD: PR7: 956 AA.
AC 000951:
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Hemolysin (Cytolysin II) (Cly-IIA) (Hly-IIA) (CYTC) (APPA).
GN APPA OR CLYIIA OR HLYIIA OR CYTC.
OS Actinobacillus suis.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OX NCBI_TaxID=716;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=3714:
RX MEDLINE=92267623; PubMed=1587585;
RA Burrows L.V., Lo R.Y.;
RT "Molecular characterization of an RTX toxin determinant from
RT Actinobacillus suis."
RL Infect. Immun. 60:2166-2173(1992).
CC -!- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A SUIS. MIGHT BE A
CC SECRETED CYTOTOXIN, POSSIBLY THE EXTRACELLULAR HEMOLYSIN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE TOXIN ONLY BECOMES ACTIVE WHEN
CC -!- PFM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M90440; AAA21918.1; -.
DR InterPro: IPR001343; Hemolysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003955; RtxA.
DR pfam: PF00353; hemolysinCbind; 1.
DR pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABDNCRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN-CALCIUM; 1.
KW Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
KW Transmembrane; Lipoprotein; Palmitate.
FT TRANSMEM 238 254
FT TRANSMEM 302 320
FT TRANSMEM 383 406
FT DOMAIN 719 799
FT REPEAT 719 724
FT REPEAT 728 733
FT REPEAT 737 742
FT REPEAT 746 751
FT REPEAT 755 760
FT REPEAT 764 769
FT REPEAT 773 778
FT REPEAT 782 787
FT REPEAT 794 799
SQ SEQUENCE 956 AA: 102453 MW: 3415PFID/ADD04365 CXC64;
Query Match 47.8%; Score 2218.5; DB 1; Length 956;
Best Local Similarity 47.5%; Pred. No. 9.4e-107;
Matches 451; Conservative 188; Mismatches 257; Indels 53; Gaps 15;

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```

QY 1 MSNINV-IKSNIOGL-----NSTKSGIKNLYLAIPKDYDQ 36
Db 1 MSKITLSLKSSLOGLKNGKNKLNGAGTTLKNGLTQGTGSHLQNGAKKILYIPQYDGG 60
QY 37 KCGTLNDFIKADELGIAEPPNHTFPAKKSVDTVNOFLSLTQGTGIAISATKLEKFLQ 96
Db 61 QONGIODLVKANDLGIEWREBSNLDLAKTSFDTQKILFTDGGIVLFAPOLDNLAK 120
QY 97 KSTKNLAVGDSVENIDKRLKASNVLTSLSPFTALAGIELDLSIKKDDAPDALAK 156
Db 121 KNP--KIGNTLSASISQNIKANVTLCGIGSILASVYSGVNLNLLQNKDPNQLAK 178
QY 157 ASDLINEIIGNLSQSTQTEAFSSOLAKLGSTISOAKGFNSIGNKLONL-NFSKTNLGL 215
Db 179 AGLELTNGLVGNASSVQVDAFAEQISKLSGHLQVNGKLGIGLSNKLQNLPLDGKASGL 238

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OY 216 EITGLISGAGFALADKNASTGKVAAGFELSNVIGNTKRAISYVLAORVAAGLST 275
DB 239 DISGLISGASAGLILADKRASTKKAAGFEFANOITGNVTKAVSSYIIIAQRAVASSLS 298
OY 276 TGAAVAALITSSIMIAISPLAFMANADKFNMANALDEFAROKRFGYDGDHLLAEYQRGV 335
DB 299 TGPAALALASVVALAVSPLNVAADKFKQADLKSKSERQKLGIDODRLADFHBRETG 358
OY 336 TIESLTTISALGAVSAAVAGVAPIALVAGYGLISGLISLEASKQMFESVA 395
DB 359 TIDASVTITINLALAIISGCVAGASGLVAGAPALLVAGVGLITTTILEYKQAMFHYA 418
OY 396 NRLQGLIEMKONGGONVFPKGDSDRYAVALANLKLFLSELNKLAEARVATITQORMD 455
DB 419 NKVDRIYEMEKH-NKVFEGQDSRLADLODMKFLINLNELOAERVALITQORMD 477
OY 456 NNIGLAGITRIGERIKSGAKVADAFEDGKRVESGNTTLDKTIIDISNSGKRTQAL 515
DB 478 NOIGDLAISRRDCKISSGKAVVDAFEQNTSPSIHPSIDNKNGLINISMTN-RKTOQV 536
OY 516 HFTSPLTAGESRRRLNGKYSYINKLAFGRVKNMOWTDEEASKLDESKVIDRVA--- 572
DB 537 LFRPTLPGEBENRERIDEGKNSYITKLHIDRVDSTVTVEDASSVDFTNVVORLAKF 596
OY 573 -----ETEGTDEIGLIVNNAKAGNDI:FGGKKNIDGGDGHDFVYSKDGEGENTVD 625
DB 597 DDAGNITTSKDTK---IIANLGAAGNDVFGVSGSTVIDGGDGHDFVYSR-GEYGALVID 652
OY 626 GTSATFAGSYIVNKKVAKGDIHYEVKKOEIRKVKRTETIQYRDELAKVGYQSTNLT 685
DB 653 AAETFEKSYSVKRYVGGSKALHETIAGHQTIVNGRREKTEIR-REDDRFHTGTVTVSL 711
OY 686 KSEVEVIGSOFNDVFKSGFNDIFHSGEGDDLDDGAGDDRLFFGSGKNDRLSGEGDDL 745
DB 712 KVEBELISQFNDIFKSGFDFVFGNGVDTIDENDDHLFGAGGDVIDGSGNNFL 771
OY 746 DGGSDVDVNLGAGNDVYIFKRGDNDTLYDGTGNDKLAFAFADANISDIEMIERTKGIIVK 805
DB 772 VCGTGNDIISGKNDIYHKTGDNDSITDGGODKLAFFSVNKLDFKFKVDSLEI- 830
OY 806 RMDHSGSINIIPRWY---TSMLOWYOSKNTDHIKTEOLLGKSGVSTISODIKITODKKD 861
DB 831 INOKGEKVIKGMFLLEDIASTVANYKAT-NDRKIEIILGKGEKITTSQVYDKLI--KEG 887
OY 862 GTVITSQELKKLADENKSOKLSASDIASSLNLKLVGSMALFGTANSVSSN 910
DB 888 NNQISAEALSKVYNDYNTSK-DRONVNSLAKLISVSGSTSSDFRNN 935

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROTYPE 8;
RX MEDLINE=93162836; PubMed=8432615;
RA Jansen R., Briaire J., Kamp E.M., Gielkens A.L.J., Smits M.A.;
RT "Cloning and characterization of the Actinobacillus
RL pleuropneumoniae-Rtx-toxin III (ApXIII) gene.";
INfect. Immun. 61:947-954(1993).
CC -1- FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY BUT SHOWS A STRONG
CC CYTOTOXICITY TOWARDS ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC -1- ACTIVITY (BY SIMILARITY).
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PTM: PALMITOYLATED BY APXIII. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch.)
CC -----
DR EMBL: X80055; CA56358.1; -
DR EMBL: X68815; CAA48711.1; -
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RtxA.
DR Pfam: PF00353; hemolysinCbind; 2.
DR Pfam: PF02382; RTX_1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 3.
KW TOXIN; Cytolysin; Cytotoxin; Repeat; Calcium; Transmembrane;
KW Lipoprotein; Palmitate.
FT TRANSMEM 248 .. 265 .. POTENTIAL.
FT TRANSMEM 275 .. 334 .. POTENTIAL.
FT TRANSMEM 372 .. 418 .. POTENTIAL.
FT DOMAIN 754 .. 759 .. 7 X REPEATS, GLY-RICH.
FT REPEAT 754 .. 759 .. 1.
FT REPEAT 763 .. 768 .. 2.
FT REPEAT 772 .. 777 .. 3.
FT REPEAT 781 .. 786 .. 4.
FT REPEAT 790 .. 795 .. 5.
FT REPEAT 799 .. 804 .. 6.
FT REPEAT 808 .. 813 .. 7.
FT REPEAT 827 .. 832 .. 8.
FT REPEAT 836 .. 841 .. 9.
FT REPEAT 845 .. 850 .. 10.
FT REPEAT 854 .. 859 .. 11.
SQ SEQUENCE 1052 AA; 112809 MW; F83AFE25A6FD8758 CRC64;

Query Match 42.2%; Score 1959.5; DB 1; Length 1052;
Best Local Similarity 42.7%; Pred. No. 2.2e-93;
Matches 426; Conservative 166; Mismatches 286; Indels 119; Gaps 19;

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QY 166 IGNLSOSTOTIEAFSSOLAKGTSIQAKGFSNKNLONL---FSKTNLGLTITGL 222
Db 197 VSNIAKGTITDAFTTQIOFNFKVLNNAKGLGCVGRQLOLNSGALSGLGLDIISLL 256
QY 223 SGISAGFALADRNASTGGKVAAGFELSNOVIGNVTAKISSYLAORVAAGLSTTGAVAL 282
Db 257 SGVTASFAFLANKNASTSTKVAAGFELSNOVIGITKRAVSYLLAQRLAAGLSTTGAVAL 316
QY 283 ITSSITLAIPLAFNMAADFNHANADEFKAKFRFGYDGHLLAEYGRVGTIEASLT 342
Db 317 IASSISLAISPLAFNADFNFRSKFGEFAERFKLGGDKLSEFYHEAGTIDASTT 376
QY 343 TSTSLAGVAGVAAVAGSAAVAPATIALVAGVTGLISGILASQAMESVAVNRLOGKI 402
Db 377 TISTALSAIAAGTAASAGALVGAFTLLVGTITGLISILERSKOPMLDHYASKGNKI 436
QY 403 LEMEKONGQNYFDKGYDSRYAAYLANNLKFLSELNKELEABRVJAITQORMDNIGELA 462
Db 437 DEMEKKY-CKNYFENGVDARHAKAFLEDSPSLSSFKNQYETEBRAVLITQORMDYIGELA 495
QY 463 GITTKGERKSKATADADEFDDKRYEAG---SNTLLAKGTIIDISNNGKKTQALHT 518
Db 496 GITTKGDKLSSGKAYVDFQEGKLEKPPDSKVVFDEPTKEIDISNS--QTSTLLKRV 553
QY 519 SPLNAGTESRRLTNKGYSYINKLFGRVKNMOVTDG--EASSKLDFSKVIR----- 570
Db 554 TPLLPPTESRRTQGTGKEITTKLVVKKDKM-VYNGVKDGAYVDYNNLQHAHISS 612
QY 571 VAETEGTDEIGLVAKAGNDIDFVGOGKMINIDGGDHRVEYSKDGFGNITVDGTSAT 630
Db 613 VARGEERYREVRLVSHLGNNGNDKVFPLAAGSAEIHAGEGHVVYYDKT-DTGLLVIDGTAKT 671
QY 631 EAGSTTVANKVARG-DIYHEVYKROETKVKRTETIQYDYELRYKG-VGYOSTDNLKRV 688
Db 672 EGRGRSVTRELSGATKILREVIKKNOKSAVGKREETLEYDYELTOSGNSNLKAHDLHSV 731
QY 689 EEVIGSOFNDVFKSGNFIDFHSCEGDDLLDGACDDRLFGGKGNRLSGDEG----- 742
Db 732 EETIGSNQDERFKSGFRIFIGABDDDLNNGDGDLLYDGKNDLGMGNDQLYG 791
QY 743 -----DLDDGSGSDV 753
Db 792 EGNDKLLGNGNNYLSGGDGNDELQVINGFVNLRGKGDKDLKYGSSGDDLLDGGCGNXY 851
QY 754 LMGAGNDVYITRKGDGNDLYD---GTGNDKLAFLADANISDMERTKEGIIYVRKND 810
Db 852 LEGCGGSDYVYRSTISGNTIYDQKSSDLDKLYLSDFSDRLVEKVDNVLRSNESS 911
QY 811 ---GSINIPRWYITSNLQVYOSNKTDKLEOLIKDGSYITSQDIKILQDKKDVITS 867
Db 912 HNGGVLTIKDWF-----KEGNKYNHKTQIYDNKGRLTAMENIGTYFRKNAPKADNLI 964
QY 868 OELKLAIDENKSOQLASDIASDLNKLVSMAFLGTA 904
Db 965 YATKE--DNES---NLSSIKTELSKIITNAGNFGVA 996

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RESULT 9
RT31_ACTPL STANDARD: PRT: 1049 AA.
AC P55130:
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE RTX-III toxin determinant A from serotype 2 (APX-IIIA) (Cytolysin
DE IIA) (CLV-IIIA).
DE APXIIA OR CLVIIA OR RTX OR PTXA.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OX NCBI_TaxID=715;
RN [1]

```

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RP SEQUENCE FROM N.A.
RC STRAIN-SEROTYPE 2:
RX MEDLINE-93263992; PubMed-8494611;
RA Chang Y.-F., Shi J., Ma D.-P., Shu S.J., Lein D.H.;
RT "Molecular analysis of the Actinobacillus pleuropneumoniae RTX
RL toxin-III gene cluster.";
RN DNA Cell Biol. 12:351-362(1993).
RP SEQUENCE OF 828-1049 FROM N.A.
RC STRAIN-1536 / SEROTYPE 2;
RX MEDLINE-95012630; PubMed-7927703;
RA Jansen R., Briatte J., van Geel A.B.M., Kamp E.M., Gielkens A.L.J.,
RA Smits M.A.;
RT "Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (ApX)
RL operons: characterization of the ApXIII operons.";
CC Infect. Immun. 62:4411-4418(1994).
CC -I- FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY BUT SHOWS A STRONG
CC CYTOTOXICITY TOWARDS ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC -I- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY (BY SIMILARITY).
CC -I- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -I- PTM: PALMITOYLATED BY APXIII. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC -----
DR EMBL, L12145; AAA1924.1;
DR EMBL, X80056; CAB3652.1; ALT_SEQ.
DR InterPro: IPR001343; Hemlyan_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003955; RTX_A.
DR Pfam: PF00353; hemolysinCbind; 2.
DR PRINTS: PRO0313; CABDNCRPT.
DR PRINTS: PRO1488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 3.
KW Toxin; Cytolysins; Cytotoxin; Repeat; Calcium; Transmembrane;
KW Lipoprotein; Palmitate.
FT TRANSMEM 154 170 POTENTIAL.
FT TRANSMEM 315 331 POTENTIAL.
FT TRANSMEM 397 413 POTENTIAL.
FT DOMAIN 753 858 11 X REPEATS, GLY-RICH.
FT REPEAT 753 858 1.
FT REPEAT 762 767 2.
FT REPEAT 771 776 3.
FT REPEAT 780 785 4.
FT REPEAT 789 794 5.
FT REPEAT 803 803 6.
FT REPEAT 807 812 7.
FT REPEAT 826 831 8.
FT REPEAT 835 840 9.
FT REPEAT 844 849 10.
FT REPEAT 853 858 11.
SQ SEQUENCE 1049 AA; 112491 MW; F99846BFD4E5CE72 CRC64;

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Query Match

Best Local Similarity 43.1%; Score 1928; DB 1; Length 1049;

Matches 429; Conservative 152; Mismatches 295; Indels 120; Gaps 21;

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QY 8 KSNIOAGLNSTRSGKL-----NLVLAIPKDYDPQKGTGLNDFI 45
Db 19 KROVKKGVDTYTKNGLDVGSQAKLQALAGKAVQKTKLVLYIPREYDGSVGNQGFPLV 78

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QY 46 KADELGIARLAEPNHTETAKSVDTVNOFLSTOTGIATSATKLEFKLOKHSNKLAK 105
DB 79 KAADELGIQVYVNRNNELEVAHKSLSGTADQFLGLTERGLTFLAPDLDFLOKHSXSNV 138
QY 106 GLDSEVNIIDRLKASVNIITLSSFLGTALAGIELDSIKKGDAPADPAALAKASIDLINEL 165
DB 139 GSSSTGDVNS-KLASSQTIISGIVGLVLAGININENIISGSGLE-LAERGVSILASEL 196
QY 166 IGNSOSTOTTEAFSSQIATLGSTISQAKGFSNIGKLNQNN--FSKTNLGLTITGL 222
DB 197 VSNIAKGTITIDAFITTOIIONFGKLAENAKGLGVCORQIONISGSLXKTXGLDIISLL 256
QY 223 SGISAGFLADKNASTGCKKVAAGELSNQVIGNTKAISSVLAQRAVAGSTTGAAVAL 282
DB 257 SGVTRSEFLRNKNASTSTKVAAGELSNQVIGITKVAASYILQRLVAGLSTGPAAL 316
QY 283 ITSSIMLAISPLAEMNADKFNHANAIDDEFKOFKFEYDGDHLLAEQORVGTIEAST 342
DB 317 IASSISLAISPLAFLRVADNENRSKEIGEFARFKLGYDDDKLSEFYHAGTIDASTIT 376
QY 343 TISTALGAVSAGVAANAAGVAPIALLVAGVTGLISGLLEASKQAFESVANRLQKI 402
DB 377 TISTALSAIAGTAASAGALVAPITLVTGTLGSLIGLEFSKQPLDHVASKIKKI 436
QY 403 LEWEKONGGONYEPDKGYDSRYAVALIANNLKFLSELNKELEARIATIQORWNNIGLA 462
DB 437 DEMEKKY-GKNYFENGIDARKAFLEDSFLLSSPNQYETERAVLTIOQRWDEXIGLA 495
QY 463 GITRLGERIKSGAVAAAFEDGKVEAG---SNITLDKAGIIDISNSNKKTOALFT 518
DB 496 GITKQKGLSSGKAVYDFQSGKLEKKPDPFSKVPPTGCEIDISNS--QTSILKFV 553
QY 519 SPLLTAGTESERLITNGKYSTINKIKGRVKNMOVTDG--EASSKLFESVIOQ----- 570
DB 554 TPLLTGPESEREFOTQGYEYITKLIVYGKDKM--VNVNCKGKAVYDTNLIOHAHSS 612
QY 571 VAHEGTEDEGLIVNAGANDIFVGGCKMIDGGDGHDRFYSGDGFQIYVDGTSAT 630
DB 613 VARGEERYEVALVSHLNGNDKVLFLAGSARIEHAGEGDVYVYKT--DTGLLVTDGTAT 671
QY 631 EAGSYTVNRKVAARG-DIYHEVYKROETFKVKTETIQYRDYELRRKV--YGYSTDNLKSV 688
DB 672 EGRKSVYTRRELSGATKILREVYIKNOKAVAGREFTLEYRDELQVLOSQSNLKADELHAY 731
QY 689 EEVIGSQPNDFKSGKENDITFHSGBDDLDCGAGDRLFCGKGNDRISG----- 739
DB 732 EE-IGSNQREDFKSGKFRDIFHGADDDLNGNDGDDILYDKGNDELKRGNDQLYGG 790
QY 740 EGD-----DILLDGGSGDDV 753
DB 791 EGDKLLGNGNNYLSGGDGDDELQVLAGNFPNVLRGKGDKLKYSSGSDLLDGGEGNDY 850
QY 754 LMGAGNDVYIFRKGDGNDTLYD---GTGNDKLAFAADANISIDIMIERTEKGIYK--RND 808
DB 851 LEGDGDSEFYVYRSTGSHHTIYDQKASDSKXLVLSLDSFNLILYKRVNDELFRSNNS 910
QY 809 HSGSINIPRWYITSNLQNYGSKTDHKLIEQIGKDGSTISDQIDKILQDKKDTVITSQ 868
DB 911 NSGVLTJTKDWEKGNSTY-----HKIEQIVDKNGRKLTAGNLCNNFHD---TQOASS 959
QY 869 ELKKLADENSKOKLASDIASSLINKLVGSMALFETA 904
DB 960 LKKNVTOEONESNLSS--LKTGLCKITTMAGNFGVA 993

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DE Hemolysin, plasmid.
GN HTYA.
OS Escherichia coli.
OC Plasmid Incir2 phly152.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Hess J., Wels W., Vogel W., Goebel W.;
RT "Nucleotide sequence of a plasmid-encoded hemolysin determinant and
its comparison with a corresponding chromosomal hemolysin sequence.";
RL FEMS Microbiol. Lett. 34:1-11(1986).
RN [2]
RP PALMITOYLATION OF LYS-564 AND LYS-690.
RX MEDLINE=9509325; PubMed=7801126;
RA Stanley P., Packman L.C., Koronakis V., Hughes C.;
RT "Fatty acylation of two internal lysine residues required for the
toxic activity of Escherichia coli hemolysin.";
RL Science 266:1992-1996(1994).
RN [3]
RP PALMITOYLATION OF LYS-564 AND LYS-690.
RX MEDLINE=96404790; PubMed=8808931;
RA Ludwig A., Garcia F., Bauer S., Jarchau T., Benz R., Hoppe J.,
RA Goebel W.;
RT "Analysis of the in vivo activation of hemolysin (HTYA) from
Escherichia coli.";
RL J. Bacteriol. 178:5422-5430(1996).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
DEFINED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.
CC -1- PTM: PALMITOYLATED BY HTYC. THE TOXIN ONLY BECOMES ACTIVE WHEN
MODIFIED.
CC -1- DISEASE: THE HEMOLYSIN OF E. COLI IS PRODUCED PREDOMINANTLY BY
STRAINS CAUSING EXTRAINTestinal INFECTIONS, SUCH AS THOSE OF THE
URINARY TRACT.
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC
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CC
EMBL: M14107; AAA98233.1; -
DR InterPro: IPR001343; HemLysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RtxA.
DR Pfam: PF00353; hemolysinCbind; 2.
DR Pfam: PF02362; RTX_1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 4.
KW Hemolysin; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
KW Transmembrane; Lipoprotein; Palmitate; Plasmid.
FT TRANSMEM 238 260
FT TRANSMEM 268 327
FT TRANSMEM 365 411
FT DOMAIN 724 870
FT REPEAT 724 729
FT REPEAT 724 729
FT REPEAT 733 738
FT REPEAT 742 747
FT REPEAT 751 756
FT REPEAT 760 765
FT REPEAT 769 774

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FT REPEAT 778 783 7.
FT REPEAT 787 792 8.
FT REPEAT 796 801 9.
FT REPEAT 807 812 10.
FT REPEAT 817 822 11.
FT REPEAT 826 831 12.
FT REPEAT 835 840 13.
FT REPEAT 844 849 14.
FT REPEAT 856 861 15.
FT REPEAT 865 870 16.
FT LIPID 564 564 PALMITATE.
FT LIPID 690 690 PALMITATE.
SQ SEQUENCE 1024 AA; 110201 MM; 83944917F76C945B CRC64;

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Query Match 39.98; Score 1852.5; DB 1; Length 1024;
 Best Local Similarity 41.58; Pred. No. 6,6e-88;
 Matches 426; Conservative 154; Mismatches 307; Indels 139; Gaps 24;

```

QY 7 IKSNIQAGL-----NSTKSGLK-----NLVLAIPRDYDPOKGGTLNDF 44
DB 9 IKSTLOSASOAAANKLHSGQSTKDALKKAEDTRNAGNRLILLIPDYKGG-GSSLNDL 67
QY 45 IKADELGIARLAEPNHTETAKSVYVNOFLSTQTGTATSAITKLEFLQKH--STNK 102
DB 68 VRTADELGEIVQYDEKNGTAITQVFTAKELIGTERGVITAPOLDKILQYKAGNI 127
QY 103 LAKGLDSVENIDRLKAKASNVSTLSSFLGTALAGIELDSLKK---GDAFDALAKAS 158
DB 128 LGGG---AENIGDNLGKAGIILSTFQNFITGALSMMKIDELIKKOKSGVSSSELAKAS 184
QY 159 IDLINEILGNLSQTQTEAFSSQLAKISTISQAKGFSNIGKLNUL-NFSKTNGLLEI 217
DB 185 IELINQVPTVASLNNVNSFSQQLNTLTSVSLTKHLGVGNKLDLPLNDINIGAGLDT 244
QY 218 ITGLLSGISAGFALADKNASTGKVAAGELNOVIGNYKAISVLAQRYAGLSTTG 277
DB 245 VSGIISAIASFTLSNADADTRTKAAAGVELTKVLGNNGKGSQYIIQRAAGLSTSA 304
QY 278 AVALITSSIMLAISPLAFMNAADKFNHNAALDEPAKORFKFGYDGDHLIAEYQRGVGTI 337
DB 305 AAAGLILASAVTLAISPLSFLSIADKFRANKIEYQRFKILGDDSLIAAFHKEGTAL 364
QY 338 EASLTITISALGAVSAGVSAAGAVGAPIALLVAGVGLISGILEASQAFESVANKR 397
DB 365 DASLTITISVLAIVSSGISAAATTSLVGAPVSAVGVIIISGILEASQAFEHVASK 424
QY 398 LQKILEEMKONGQVYFPKGYDSRYAAYLANMLKELSELKLEAEERYAITQQRWNN 457
DB 425 MADVIAMWEKKH-GKNYFENGIDARHAAPLEDNFKILSOVKEYSVERSVLITQOHMDL 483
QY 458 IGLGLITYLGERIKSGKAYADAEPDGKAYEAGSN---ITLDAKTIIDISNSNGKKTQ 513
DB 484 IGLGLAVTNGDKTSLGKSYIDYEKGKRLKXKDEFQKQVDFPLKGNIDLSDS--KSSP 541
QY 514 ALHFTSPLLTAGESREBLNCKYYSINKLKFGRYKNNQVTD--GEASSKIDPEKVIQRAVA 572
DB 542 LKFEVPLPLTPEERERRQSGEYETITELLVKGVDMKTVKGVODGAVYDYSNLIQHAS 601
QY 573 ETEGT-DEIGLIVNARAGNDLIFVGGKKNIDGGDGHDRVFSK--GGFGNITVDGTSAP 630
DB 602 VGNNOYREIRIESHLDGDDKVFELSGANSNIYAGKHDPVYVYKTKDTGY--LTIIDETKAT 659
QY 631 EAGSYVNVKRVARGD--IYHEVVKROETVYKRTETIYQRYDELARKV-GYGYOSTDNLKS 667
DB 660 EAGNYVIVTR-VLEGDVKVLQVEVVKKEQEVSGKTEKTYRSEYFTIINGKNILETDLVS 718
QY 688 VEEVVISQFNDVFKSGKFNIDPHSGEGDDLLOCGAGDDR-----726
DB 719 VEEILGTTRADKPFSGKFTDIFHGADGDLLEBNDGNDRLRYGDKGNDPLSGGNDQLYG 778
QY 727 -----LFGGKGNDRLSGEGDDLLOCGAGSG 750

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DB 779 GDCNDKLIQVAGNNYILNGGDDDEFQVQNSLAKNVLFGGKGNDKLYGSEGADLLDGE 838
QY 751 DDVLNGAGNDVYIFRKQDGNLDLYOCTG-NDKLAFPADAMISIMIERTEGIIYKRN- 808
DB 839 DDLKGGYGMIDYRYSGLYHHIIDDGKEKDLSLADIDFROVAFREKENDLIMTKGEG 898
QY 809 -----HSGSINIPRWITNSLQNYOSNKTDKHIEQLIGDGSYITSQDIDKILQDKK-- 860
DB 899 NVLSIGHKNQITFRNMF-----EKESGDINHEIEQIFDKSGRIITPDSLKKALEYQQRN 953
QY 861 -----DGVYITSQ-----ELKRLADENKSQKLSASDIASSLNKLVGSMALFPT 903
DB 954 NKASYVGNDALAYVSGQDNLPLNEISKITSAGSPDYKEERTASLQLSGNASDFSY 1013
QY 904 A-NSVS 908
DB 1014 GRNSIT 1019

RESULT 11
HLX1_ECOLI STANDARD; PRT; 1023 AA.
ID HLX1_ECOLI
AC P09983;
DT 01-MAR-1989 (Rel. 10, Created)
DI 01-MAR-1989 (Rel. 10, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Hemolysin, chromosomal.
GN HLX1.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=J96 / SEROTYPE O4;
RA MEDLINE=85234404; PubMed=3891743;
RX Felmlee T., Pellett S., Welch R.A.;
RT "Nucleotide sequence of an Escherichia coli chromosomal hemolysin.";
RL J. Bacteriol. 163:94-105(1985).
RN (2)
RP SEQUENCE OF 1-44 FROM N.A.
RC STRAIN=2001;
RX MEDLINE=85258115; PubMed=3894051;
RA Nicoud J.-M., Mackman N., Gray L., Holland I.B.;
RT "Characterisation of HlyC and mechanism of activation and secretion
of hemolysin from E. coli 2001.";
RL FEBS Lett. 187:339-344(1985).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
DEFINED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.
CC -1- PTM: PALMITOYLATED BY HLYC. THE TOXIN ONLY BECOMES ACTIVE WHEN
MODIFIED.
CC -1- DISEASE: THE HEMOLYSIN OF E.COLI IS PRODUCED PREDOMINANTLY BY
STRAIN CAUSING EXTRAINTestinal INFECTIONS, SUCH AS THOSE OF THE
URINARY TRACT.
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See http://www.isb.ch/announce/
or send an email to license@isb-sib.ch).
CC EMBL: M10133; AAA23975.1; -
CC EMBL: X02768; CAA26546.1; -

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DR PTR; A24433; LEECA.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR InterPro: IPR003995; RTX_A.
 DR Pfam: PF00353; hemolysincabind; 2.
 DR Pfam: PF02382; RTX_1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PRINTS: PR01488; RTXTOXIN.
 DR PROSITE: PS00330; HEMOLYSIN_CALCITON; 4.
 DR Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
 KM Transmembrane; Lipoprotein; Palmitate.
 FT TRANSMEM 237 259 POTENTIAL.
 FT TRANSMEM 267 326 POTENTIAL.
 FT TRANSMEM 364 410 POTENTIAL.
 FT DOMAIN 723 869 16 X REPEATS, GLY-RICH.
 FT REPEAT 723 728 1.
 FT REPEAT 732 737 2.
 FT REPEAT 741 746 3.
 FT REPEAT 750 755 4.
 FT REPEAT 759 764 5.
 FT REPEAT 768 773 6.
 FT REPEAT 777 782 7.
 FT REPEAT 786 791 8.
 FT REPEAT 795 800 9.
 FT REPEAT 806 812 10.
 FT REPEAT 816 821 11.
 FT REPEAT 825 830 12.
 FT REPEAT 834 839 13.
 FT REPEAT 843 848 14.
 FT REPEAT 855 860 15.
 FT REPEAT 864 869 16.
 FT LIPID 563 563 PALMITATE (BY SIMILARITY).
 FT LIPID 689 689 PALMITATE (BY SIMILARITY).
 FT VARIANT 6 A->T (IN STRAIN 2001).
 SO SEQUENCE 1023 AA; 109867 MW; 196D5C0A9A28B54D CRC64;

Query Match 39.8%; Score 1849; DB 1; Length 1023;
 Best Local Similarity 41.7%; Pred. No. 9.9e-88;
 Matches 429; Conservative 154; Mismatches 306; Indels 140; Gaps 25;

QY 7 IKSNTQAGL-----NSTKSGLK-----NLTLAPKRYDPQKGTLMDF 44
 DB 9 IKSSTQSAKOSANKLHNSAGSTKDALKKAAQOTRNAGNRLLLLPKRYKGG-GSLMDL 67
 QY 45 IKADELGIARLAEPNPHETAKKSVDFVNOPLSTQGTIAISATKLEKFLQKH--STNK 102
 DB 68 VRTADELGIEVOYDEKNGTAITKQVFGTAKEKILGTERGVTFAPQDLKLLQKQKAGK 127
 QY 103 LAKGLDSVENIDRKLGKASNVLSLSSFLGTALAGIELDSLKK---GDAAPDALAKS 158
 DB 128 LG---GSAENIGDNLGKASVLSFTQNFGLTALSSMKIDELKKQSGGNVSSSELAKS 184
 QY 159 IDLINEITGNLSQSTOTIAFSSQLAKISTISOAKGFENINCKLONL-NFSKTNLGEI 217
 DB 185 IELINOLV-DTAAASLNNVVSFOQNLKLSVLSNTHLGVGNKLNLPNLNIGAGLDT 243
 QY 218 ITGLISGASGAFALADKNASTGKVAAGFELSNQVIGNYTKAIISSVYLAQRYAAGISTG 277
 DB 244 VSGIISAIASFLSNADDTGKKAAGVLTITKVLGVNGKISQYIIQRAAQGLSTSA 303
 QY 278 AVALITSSIMAIISPLAFMNAADKFNHANAIDEFKAKQFRKRGYDGDHLAEYQKRGVGI 337
 DB 304 AAGGLIASVYTLAISPLSFLSIADKFKFRANKIEEYSQRFKKLGYDDSDSLAFAHKETGA 363
 QY 338 EASLTIITRALGAVSAGVSAANGAVCAPIALLVAGVGLISGLEAKQAFESAVNR 397
 DB 364 DASLITRISYVLASVSSGISAAATSLVGAIVSALVAGVGLISGLEASQAQFEHVAASK 423
 QY 398 LQKTIEMEKONGCONVFDKGYDSRYAAYLANNIKFLSELNKLAEERVAITQQRWNN 457
 DB 424 MALVIAEMEKH-GKNYFENGIDARHAPLEDFNFKTILSYNKEYSVRSVLLITQHWDTL 482

QY 458 IGLAGITKIGERIKSGKAYADAFEDGKKVEAG---SNTILDARTGIIDISNSNGKTQ 513
 DB 483 IGLAVTNRNGDKTLSSKRTIDYIEGKRLEKKPDEFQKQVDPDLKGNLIDLSDS--KSS 540
 QY 514 ALHETSPLLTAGTESKRELTNGKYSTINKLKGRKAKNNQVTD-GEASSKLSKTYQRYA 572
 DB 541 LKFTVPLPLTPGEIEREROSGKEYETITELVKGDKWTVKGVQKGSYYDLSNLIQHS 600
 QY 573 ETEGTT-DEGLIYNAKAGNDLFEVGGKMNIDGGDGHDFVFSK-DGCFGNITVDGTSAT 630
 DB 601 VGNNOYREIRIESHLDGDKVFLSAGSANITAGKCHDVYVDKPDYGV--LTIQTKAT 658
 QY 631 EAGSYTVNRKVRKD--IYHEVVKROETVGRKTEFTIYRDYELRKV-GYQSTDNLS 687
 DB 659 EAGNYTVTR-VLGGDVKVLQEVVKEQEVSGKTEKTYRSEYFTHINKNLTETDNLS 717
 QY 688 VEEVIGSQFNDVFKGKFNDFPHSGGDDLLDGGAGDRLF----- 728
 DB 718 VEEIIGTRADKFFGSKFADIFHGADGDHIEGNDNDRLXGKGNLTLSGGNGDQLYG 777
 QY 729 -----GKGNDRLSGBGDDLLDGGSG 750
 DB 778 GGGNDKLIGGANNVILGGDDDELQVQNSLAKNVLSGGKGNKLYSGEGADLLDGGEG 837
 QY 751 DDVINGAGNDVYIFRKGDDNDLIDGTG-NDKLAFAADANISIMIERTEGIVTRND- 808
 DB 838 NDLLKGGYNDIYRYSLSGHHIIDDGKDDLSLADIDFVYARREBNDLIMYKAB 897
 QY 809 -----HSGSINIPRWYITSNLTQYNSKTDHKIEQLGKGSYITSQIDKLLQDK-- 860
 DB 898 NVLSIGKNGITTFKNMF-----EKESGDISNHQIEQIFDKDGVITPDSLKALEVOQS 952
 QY 861 -----DQTVITTSO-----ELUKLADENKSKOGLSASDIASSLNVSMALFCT 903
 DB 953 NKASYVGNDAALAYSGOGNINPLINEISKIISAAGNDVKEERAAASLLQLSGNADSFY 1012
 QY 904 A-NSVSSNA 911
 DB 1013 GRNSTITLTA 1021

RESULT 12
 RT12.ACTPL STANDARD; PRT; 1023 AA.
 AC P55129;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE RTX-I toxin determinant A from serotypes 5/10 (APX-IA) (Hemolysin IA)
 DE (HLY-IA) (Cytolysin IA) (CLY-IA).
 GN APXIA OR CLYIA OR HLYIA.
 OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Actinobacillus.
 OX NCBI_TaxID=715;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13039 / SEROTYPE 10;
 RC MEDLINE=94276858; PubMed=8007819;
 RX Nagai S., Yagihashi T., Ishihama A.;
 RA "DNA sequence analysis of an allelic variant of the Actinobacillus
 RT pleuropneumoniae-RTX-toxin I (ApXIA) from serotype 10.";
 RL Microb. Pathog. 15:485-495(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K17 / SEROTYPE 5;
 RC MEDLINE=96401417; PubMed=8807793;
 RA Chiu N., Frey J., Chang C.F., Chang Y.F.;
 RT "Identification of a locus involved in the utilization of iron by
 RL Actinobacillus pleuropneumoniae.";
 RN FEMS Microbiol. Lett. 143:1-6(1996).
 RP [3]
 RP SEQUENCE OF 886-1023 FROM N.A.

30-MAY-2000 (Rel. 39, last annotation update)
DE RTX-I toxin determinant A from serotypes 1/9 (APX-IA) (Hemolysin IA)
CN AEXIA OR CLYIA OR HLYIA.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
ON NCBI_TaxID=715;
RX MEDLINE=91348845; PubMed=1879928;
RA Frey J., Meier R., Gysi D., Nicolet J.;
RT "Nucleotide sequence of the hemolysin I gene from Actinobacillus
pleuropneumoniae.";
RL Infect. Immun. 59:3026-3032(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S 4074 / SEROTYPE 1;
RX MEDLINE=94237497; PubMed=8181764;
RA Frey J., Haldimann A., Nicolet J., Boffini A., Prentki P.;
RT "Sequence analysis and transcription of the apxi operon (hemolysin I)
from Actinobacillus pleuropneumoniae.";
RL Gene 142:97-102(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ISOLATE CYT 13261 / SEROTYPE 9;
RX MEDLINE=93366425; PubMed=8339691;
RA Jansen R., Briatore J., Kamp E.M., Gielkens A.L.J., Smits M.A.;
RT "Structural analysis of the Actinobacillus pleuropneumoniae-RTX-toxin
I (Apxi) operon.";
RL Infect. Immun. 61:3688-3695(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S 4074 / SEROTYPE 1;
RX Chang Y., Wang Y., Chin N.;
RT Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
RL "-1 FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.PLEUROPNEUMONIAE,
WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTOXIC FOR
ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC "-1 DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
ACTIVITY.
CC "-1 DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC "-1 PTM: PALMITOYLATED BY APXIC. THE TOXIN ONLY BECOMES ACTIVE WHEN
MODIFIED (BY SIMILARITY).
CC "-1 MISCELLANEOUS: APXIA IS PARTIALLY DELETED IN SEROTYPES 2, 4, 6, 7,
8, 12, AND TOTALLY DELETED IN SEROTYPE 3.
CC "-1 MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF SEROTYPE 1.
CC "-1 SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X52899; CAA37081.1; -
DR EMBL: X68595; CAA48586.1; -
DR EMBL: X73117; CAA51548.1; -
DR EMBL: U05042; AAB05034.1; -
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RTX_A.
DR Pfam: PF00335; hemolysincbind; 2.
DR Pfam: PF02382; RTX_1.
DR PRINTS: PRO0313; CABNONGRP.
DR PRINTS: PRO1488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 2.

KW Hemolysin; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
KM Transmembrane; Lipoprotein; Palmitate.
FT TRANSMEM 226 326
FT TRANSMEM 297 326
FT TRANSMEM 367 406
FT DOMAIN 722 845
FT REPEAT 722 727
FT REPEAT 731 736
FT REPEAT 740 745
FT REPEAT 749 754
FT REPEAT 758 763
FT REPEAT 767 772
FT REPEAT 776 781
FT REPEAT 785 790
FT REPEAT 794 799
FT REPEAT 813 818
FT REPEAT 822 827
FT REPEAT 831 836
FT REPEAT 840 845
FT REPEAT 849 854
FT REPEAT 862 867
FT REPEAT 877 882
SQ SEQUENCE 1023 AA; 110193 MW; F99A88CFC9F1A598 CRC64;
Query Match 37.2%; Score 1727; DB 1; Length 1023;
Best Local Similarity 39.8%; Pred. No. 1,8e-81;
Matches 399; Conservative 180; Mismatches 308; Indels 116; Gaps 28;

QY 8 KSNIGAGLNTKSGSL-----KNVIAIPKDVDPQKGGTINFIKADELGIARLAEPP 60
DB 21 KSAKSGAGALKNGLGVOKAGOKLITLIPKDVDPQKGGTINFIKADELGIARLAEPP 80
QY 61 NHTFAKSVDTYNOFLSTOTGTIAISATKLEFLQHSYTNKLAKGL-DSEVNIIDKRLG 119
DB 81 NGTALAEELGTTPKLLGFSERGALFAPQFDKLNN--OKLSKSGSSSEALGQRLNK 138
QY 120 ASNVLSLSTSLFGTALAGIELDSLTKR---GDAAPALAKASIDILINELTIGMLSGSTOR 175
DB 139 TQTLASLQSLGTALAGMDLSLRRRNGEDVSGSELAKGLAOLVNDINASTGT 198
QY 176 TEARSSOLAKGS---TTSQAKGFSNIGNKLONL-NFSKTNLGLLEITGLLSISAGFAL 231
DB 199 VDAFBEOLGKLAMPYLTLA-----LSGLASKUNLPDLISLGGPDVAGSILSVASAFIL 254
QY 232 ADKNASTGKYVAGFELSNQYIGVNTKAISSYVLAQRYAAGLSTGVAALLTSSILAI 291
DB 255 SNKDADAGTKAAAGIEISTKILGNIKNAVSOYIIAORVAAGLSTGATGGLISVVALAI 314
QY 292 SPLAFMNAADPFNNANLDEFKAPRKRGYGDHLLAEYRGVGTIRASLTITSTALGAV 351
DB 315 SPLSLNVAADFERAKOLEYSEKPKRGYGDHLLAEYRGVGTIRASLTITSTALGAV 374
QY 352 SAGYSAAGVAGVAPIALVAVGTGLISGLEASKQAMFESVANKLOGLKLEBKONG 411
DB 375 SAGVGAATAGSIVGAPVALVATIGTILGILDSKQAFERVAATKLAKIDEKKH-G 433
QY 412 QNYFKGYSRKAATLANNLKFLSELNKEDEARVATITQORWNNNGELAGITKLERI 471
DB 434 KNYFENGVDARSALFELTFFELLSQYKSEYERVAATITQORWNNNGELAGITRKSQDT 493
QY 472 KSGRAYADAFEDGKRYEAG---SNITLDAKTGIIIDISNSNGKRTQALHTSPLLTNGTE 527
DB 494 KSGRAYVDFEFGKLEKEPRFDKVPDELEKIDLSIN--KTLTLKFYTPVFTAGEE 551
QY 528 SRERLTNGKSYINKLKFGRYAKNMQVYTGDEASSKL-DESKYIQRAEFGDELGLYNA 586
DB 552 IREKQOTGYQYVTELFYKGEKEKVVTVGOSHNAIYDTNLIQLAIDKRG-EKQVTTES 610
QY 587 KAG--NDLFFVQGGKMNIDGGDGHVRVFSK-DGSGFNGITVDTGTSATGAGSYTVNRKV-A 642
DB 611 HUGENKRIYLVSSGSIYVAGNGHDVAIYDKTDITG--LTFGGSAQAKAGEYIVKELKA 668


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QY 529 RERLTNGKYSYINKLKFGRVKNMOTVTDGEASSKL-DESKYIOR-VAETEGTDEIGLTVNA 586
RT 555 RKTRQSGKYEFTTELKAKGRTDMKVCVPNSNGYDESNLIQHVAFTDNKVFLEARLIANL 614
DB 587 KAGNDIFVQGGKMNIDGCGHDFRFTSKDGFNITVDGTSATEAGSYVYVKNVAGDI 646
QY 615 GAKDDYVFEVSGSTIVAGGQDVVADYSK-GRGALYIDGRNMAKQAYKVERDLSTQV 673
DB 647 YHEVVKQETKRGVKTETIYRDVEL--RKVGYGOSTDNLSKEEYVIGSOFNFVFGSK 704
QY 674 LQETVSKQETKRGVKTETIYRDVEL--RKVGYGOSTDNLSKEEYVIGSOFNFVFGSK 733
QY 705 FNDIFHSGECDL-----LDGAGADRLF----- 728
DB 734 FNDVFEHGHGDGLLYVDGDDRLYGDNQNDIEHGGQGNLKYGAGNDRLFEGEYNNVLD 793
QY 729 -----GKGNDRLSGDEGDDLLDGGSGDDVYNGAGNDVYIFRKGDDG 770
DB 794 GGEEDHLEGGNGSDILRGSGNDKLEGNQDDLLDGGEGDDQLAGEGNDIYVYRKEYG 853
QY 771 NDLYTDTGN-DKLAFADANSDIMIERTEKGLIVKRNDHSGSINIPRWYTSN---LQ 825
DB 854 HHTTSHGDKDKLSANINKDVSEFRNGNDLKTNNRT-AVTFKGFSPKSPSSAGLD 912
QY 826 NYOSNKTDKHLEQLIGKDGSYTSDQIDKILQDKRKGVTYSOELKRLA 874
DB 913 EYQKLEAVEP---KD---VHDLRDNLSYSEVKSTNHSIIKLKLS 953

RESULT 15
CYAA_BORPE STANDARD; PRT; 1706 AA.
ID CYAA_BORPE STANDARD; PRT; 1706 AA.
AC P15318;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Bifunctional hemolysin-adenylate cyclase precursor (Cyclolysin) (ACT)
DE (AC-HLY) [Contains: Calmodulin-sensitive adenylyl cyclase
DE (RC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl cyclase); Hemolysin].
GN CYA OR CYAA.
OS Bordetella pertussis.
OC Bordetella; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=18323;
RX MEDLINE=88216178; PubMed=2897067;
RA Glaser P., Ladant D., Sezer O., Pichot F., Ullmann A., Danchin A.;
RT "The calmodulin-sensitive adenylyl cyclase of Bordetella pertussis:
RT cloning and expression in Escherichia coli.";
RT Mol. Microbiol. 2:19-30(1988).
RN [2]
RP SEQUENCE OF 1489-1706 FROM N.A., AND BIFUNCTIONAL PROTEIN DESCRIPTION.
RC STRAIN=18323;
RX MEDLINE=89091151; PubMed=2905265;
RA Glaser P., Sakamoto H., Bellalou J., Ullmann A., Danchin A.;
RT "Secretion of cyclolysin, the calmodulin-sensitive adenylyl cyclase-
RT haemolysin bifunctional protein of Bordetella pertussis.";
RT EMBO J. 7:3997-4004(1988).
RN [3]
RP DOMAINS.
RX MEDLINE=91177021; PubMed=2007407;
RA Munier H., Gilles A.-M., Glaser P., Danchin A., Sarfati R., Barzu O.;
RT "Isolation and characterization of catalytic and calmodulin-binding
RT domains of Bordetella pertussis adenylyl cyclase.";
RT Eur. J. Biochem. 196:469-474(1991).
RN [4]
RP MUTAGENESIS.
RX MEDLINE=89251630; PubMed=2542030;
RA Glaser P., Elmaoglou-Lazaridou A., Krin E., Ladant D., Barzu O.,
RA Danchin A.;

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RT "Identification of residues essential for catalysis and binding of
RT calmodulin in Bordetella pertussis adenylyl cyclase by site-directed
RT mutagenesis.";
RT EMBO J. 8:967-972(1989).
RN [5]
RP MUTAGENESIS.
RX MEDLINE=91266896; PubMed=2050107;
RA Glaser P., Munier H., Gilles A.-M., Krin E., Porumb T., Barzu O.,
RA Sarfati R., Pellequer C., Danchin A.;
RT "Functional consequences of single amino acid substitutions in
RT calmodulin-activated adenylyl cyclase of Bordetella pertussis.";
RT EMBO J. 10:1683-1688(1991).
RN [6]
RP REVIEW.
RX MEDLINE=93119764; PubMed=8418825;
RA Danchin A.;
RT "Phylogeny of adenylyl cyclases.";
RT Adv. Second Messenger Phosphoprotein Res. 27:109-162(1993).
RN [7]
RP PALMITOYLATION OF LYS-983.
RX MEDLINE=95025937; PubMed=7939682;
RA Hackett M., Guo L., Shabanowitz J., Hunt D.F., Hewlett E.L.;
RT "Internal lysine palmitoylation in adenylyl cyclase toxin from
RT Bordetella pertussis.";
RT Science 266:433-435(1994).
RN [8]
RP PALMITOYLATION OF LYS-860.
RX MEDLINE=99214144; PubMed=10196151;
RA Basar T., Havilioek V., Bezonskova S., Halada P., Hackett M., Sebo P.;
RT "The conserved lysine 860 in the additional fatty-acylation site of
RT Bordetella pertussis adenylyl cyclase is crucial for toxin function
RT independently of its acylation status.";
RT J. Biol. Chem. 274:10777-10783(1999).
RN [9]
RP FUNCTION: THIS ADENYLYL CYCLASE BELONGS TO A SPECIAL CLASS OF
RP BACTERIAL TOXIN. IT CAUSES WHOOPING COUGH BY ACTING ON MAMMALIAN
RP CELLS BY ELEVATING CAMP-CONCENTRATION AND THUS DISRUPTS NORMAL
RP CELL FUNCTION.
CC -1- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY HOST CALMODULIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY (BY SIMILARITY).
CC -1- PTM: RELEASED IN A PROCESSED FORM.
CC -1- PTM: PALMITOYLATED BY CYAC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED IN POSITION LYS-983.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO ADENYLYL CYCLASE
CC CLASS-2 FAMILY.
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE RTX
CC PROKARYOTIC TOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: Y00545; CA68613.1; -
DR EMBL: X14199; CA32411.1; -
DR EMBL: A07292; CA00653.1; -
DR EMBL: A14850; CA01202.1; -
DR PIR: S00893; OYBRC.
DR PIR: S09403; S09403.
DR InterPro: IPR001343; Hemolysin_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RTX_A.
DR Pfam: PF00353; hemolysinCaBind; 5.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CAMDNGRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CALCITUM; 5.

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QY 856 LQDKKDGTV 864
Db 1279 MGOGGDDTV 1287

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Search completed: September 11, 2002, 09:01:54
Job time: 277 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2002, 04:16:55 : Search time 4960.61 Seconds
(without alignments)
11744.418 Million cell updates/sec

Title: US-09-884-696-1

Perfect score: 2784
Sequence: 1 atgtccaataataatgaat.....tttggctccaagtgttag 2784

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

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2: gb_hlg:*
3: gb_in:*
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6: gb_pal:*
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8: gb_pl:*
9: gb_pr:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
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17: em_hum:*
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27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgc_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Score Match Length DB ID Description

1	2784	100.0	2784	1	AF205359	AF205359 Moraxella
2	815.6	29.3	3311	6	AR104900	AR104900 Sequence
3	815.6	29.3	3311	6	I33956	I33956 Sequence 1
4	815.6	29.3	6852	1	AF314503	AF314503 Mannheim
5	815.6	29.3	7801	1	PASAILKT	M20730 Pasteurella
6	814.6	29.3	6958	1	AF314523	AF314523 Pasteurel
7	814.6	29.3	6958	1	AF314524	AF314524 Pasteurel
8	814.4	29.3	2794	6	AR054439	AR054439 Sequence
9	814.4	29.3	2794	6	AR081029	AR081029 Sequence
10	814.4	29.3	2794	6	AR085997	AR085997 Sequence
11	814.4	29.3	2794	6	BD009870	BD009870 GNRH-Leuk
12	814.4	29.3	2794	6	I12257	I12257 Sequence 1
13	814.4	29.3	2794	6	I23447	I23447 Sequence 1
14	814.4	29.3	2794	6	I80029	I80029 Sequence 1
15	814.4	29.3	2794	6	I89774	I89774 Sequence 5
16	814.4	29.3	2817	6	I12265	I12265 Sequence 9
17	814.4	29.3	2817	6	I80037	I80037 Sequence 11
18	814.4	29.3	2838	6	I12264	I12264 Sequence 8
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37	802.8	28.8	7742	1	PASLTKCABD	AF314508 Mannheim
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ALIGNMENTS

RESULT	1					
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LOCUS	AF205359	2784 bp	DNA	linear	BCT 02-OCT-2001	
DEFINITION	Moraxella bovis RTX toxin (mbxa) gene, complete cds.					
ACCESSION	AF205359					
VERSION	AF205359.1	GI:15146407				
KEYWORDS						
SOURCE						
ORGANISM	Moraxella bovis.					
	Moraxella bovis.					
	Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;					
	Moraxella.					
REFERENCE	1 (bases 1 to 2784)					
AUTHORS	Angelos,J.A., Hess,J.F. and George,L.W.					
TITLE	Cloning and Characterization of a Moraxella bovis cytotoxin gene					
JOURNAL	Am. J. Vet. Res. 62 (8), 1222-1228 (2001)					
MEDLINE	21388402					
PUBMED	11497442					
REFERENCE	2 (bases 1 to 2784)					
AUTHORS	Angelos,J.A., Hess,J.F. and George,L.W.					
TITLE	Direct Submission					
JOURNAL	Submitted (15-NOV-1999) Veterinary Medicine/Epidemiology, University of California, Davis, 2108 Tupper Hall, Davis, CA 95616, USA					


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RESULT 2
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DEFINITION Sequence 1 from patent US 6096320.
ACCESSION ARI04900
VERSION ARI04900.1 GI:12818497
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 3311)
AUTHORS Potter, A., Campos, M. and Hughes, H. P. A.
TITLE Vaccines with chimeric protein comprising gamma-interferon and
leukotoxin derived from pasteurized haemolytica
JOURNAL Patent: US 6096320-A 1 01-AUG-2000;
FEATURES
source
1..3311
location/Qualifiers
BASE COUNT 1113 a 592 c 699 g 907 t
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Matches 1544; Conservative 0; Mismatches 964; Indels 60; Gaps 9;
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DEFINITION Sequence 1 from patent US 5594107.
ACCESSION I33956
VERSION I33956.1 GI:1824747
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3311)
AUTHORS Potter A., Campos M. and Hughes H.P.A.
TITLE Chimeric protein comprising an RFX-family cytotoxin and
Interferon 2 or Interferon
Patent: US 5594107-A 1 14-JAN-1997;
JOURNAL Location/Qualifiers
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Matches 1544; Conservative 0; Mismatches 964; Indels 60; Gaps 9;

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ACCESSION	AFJ314503			
VERSION	AFJ314503.2			
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SOURCE				
ORGANISM	Mannheimia haemolytica.			
	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;			
REFERENCE				
AUTHORS	1 (bases 1 to 6952)			
TITLE	Davies,R.L., Whittam,T.S. and Selander,R.K.			
	Sequence diversity and molecular evolution of the leukotoxin (lktA) gene in bovine and ovine strains of Mannheimia (Pasteurella) haemolytica			
JOURNAL	J. Bacteriol. 183 (4), 1394-1404 (2001)			
MEDLINE	21101823			
PUBMED	11157953			
REFERENCE				
AUTHORS	2 (bases 1 to 6952)			
TITLE	Davies,R.L., Campbell,S. and Whittam,T.S.			
	Mosaic Structure and Molecular Evolution of the Leukotoxin Operon (lktCABD) in Mannheimia (Pasteurella) haemolytica, Mannheimia glucosida, and Pasteurella trehalosi			
JOURNAL	J. Bacteriol. 184 (1), 266-277 (2002)			
PUBMED	11741868			
REFERENCE				
AUTHORS	3 (bases 1 to 6952)			
TITLE	Davies,R.L., Whittam,T.S. and Selander,R.K.			
JOURNAL	Submitted (18-Oct-2000) Institute of Biomedical and Life Sciences,			
	Division of Infection and Immunity, University of Glasgow, Joseph Black Building, University Avenue, Glasgow G12 8QO, Scotland			
REFERENCE				
AUTHORS	4 (bases 1 to 6952)			
TITLE	Davies,R.L., Whittam,T.S. and Selander,R.K.			
JOURNAL	Direct Submission			
	Submitted (04-Oct-2001) Institute of Biomedical and Life Sciences,			
REMARK	Division of Infection and Immunity, University of Glasgow, Joseph Black Building, University Avenue, Glasgow G12 8QO, Scotland			
COMMENT	Sequence update by submitter			
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AUTHORS	Davies,R.L., Whitlam,T.S. and Selander,R.K.				
TITLE	Sequence diversity and molecular evolution of the leukotoxin (lktA) gene in bovine and ovine strains of Mannheimia (Pasteurella) haemolytica				
JOURNAL	J. Bacteriol. 183 (4), 1394-1404 (2001)				
MEDLINE	21101823				
PUBMED	11157953				
REFERENCE	2 (bases 1 to 6958)				
AUTHORS	Davies,R.L., Campbell,S. and Whitlam,T.S.				
TITLE	Mosaic Structure and Molecular Evolution of the Leukotoxin Operon (lktCABD) in Mannheimia (Pasteurella) haemolytica, Mannheimia glucosida, and Pasteurella trehalosi				
JOURNAL	J. Bacteriol. 184 (1), 266-277 (2002)				
PUBMED	11741868				
REFERENCE	3 (bases 1 to 6958)				
AUTHORS	Davies,R.L., Whitlam,T.S. and Selander,R.K.				
TITLE	Direct Submission				
JOURNAL	Submitted (18-Oct-2000) Institute of Biomedical and Life Sciences, Division of Infection and Immunity, University of Glasgow, Joseph Black Building, University Avenue, Glasgow G12 8QQ, Scotland				
REFERENCE	4 (bases 1 to 6958)				
AUTHORS	Davies,R.L., Whitlam,T.S. and Selander,R.K.				
TITLE	Direct Submission				
JOURNAL	Submitted (04-Oct-2001) Institute of Biomedical and Life Sciences, Division of Infection and Immunity, University of Glasgow, Joseph Black Building, University Avenue, Glasgow G12 8QQ, Scotland				
REMARK	Sequence update by submitter				
COMMENT	On Oct 9, 2001 this sequence version replaced gi:11762057.				
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Db	497	TTGACGAATTTGGTGAGCAAAATTAGTCAATTTGGTTCAAAACCTACAAAATATCAAAAGCT	556
Qy	587	tctctaataagaaacaaagctgcaaaacttaaat---tcttcaaaacaaactctggtc	643
Db	557	TAGGAGACTTTTGGAGACAAACCTCAAAATATTCGGTGAGCTTGATTAACCTGGCTTGGTT	616
Qy	644	tggaaataatctcaggttctgctacaaagcattctgcgaaggttggctttagcgaataaa	703
Db	617	TAGATGTTATCTCAGGGCTATTATCGGGCGCAACAGCTGCACCTGTACTTGACAGTTAA	676
Qy	704	atgcacgcagctgcaaaaaagctgctgcaaggttgaattgaattgaattgaattgaattga	763
Db	677	ATGCTTCAACAGCGTAAAAAAGTGGGTGGGGTTTTTGATTTGGCAACCAAGCTTTGGTGA	736
Qy	764	atgtaacaaagcaatttctcatalgttttagcacaagctggtgctgctgctgctatcaaa	823
Db	737	ATATTACCAAGCCGTTCTCTTACATTATTAAGCCCAACGCTGTTCACACAGCTTATCTT	796

QY	824	ctacggtcgtgttcgtgcttaattacttcacatgaltatgtgtgcaattagtccttttg	883
Db	797	CAACCTGGCCCTGGGGTGGCTTTAATGCTTCTACGTTTCTCTCCGATTTGGCCCATTAG	856
QY	884	catttaatgaaatgcagaagaataaattcaatcagtcataatgtctctgatgagttgcaaac	943
Db	857	CATTTCGGCGGTATTGGCCGATTAATTATATCATGCGAAAAGTTTAAAGAGTTTATGCCGAC	916
QY	944	aattccgnaaatttggctatgabatgaggatcaattatctggctgnaatatacagcgtgtgttg	1003
Db	917	GCTTTAAAAAATTAGGCTATTGACGGAGTAATTTATTGCGAATAATTCAGCGGGGAACAG	976
QY	1004	gtactatgaaagttcaattactaacacaaattagaacgaattagtcgagttctctgtgtg	1063
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QY	1064	tttcgcgtgtctgtctgaagatcgtctgtgtgtgtgcacgaattgcacatagtttgcaggtg	1123
Db	1037	TGTCGTGCTGCAGCCGGCTCGTTATGCTTCAACCGATTGCTCTTATTAGATCTGGGA	1096
QY	1124	tttaagatgtatcctctggaattttagaagcgtctaaacaggaatgtttgaaggtgtg	1183
Db	1097	TTACCGGTGTAATTTCTACAGCATTTCCATATTCTTAACAAACAAATGTTTACGACAGTGG	1156
QY	1184	ctaacgctttacaaggtlaaaattttgaatgtgggaaagcaaatgtcgtcagaacttt	1243
Db	1157	CAATTAATAATTCATTACAAATAATTGTGAATTTGGAAAAAATAATACGCTAAGAACTACT	1216
QY	1244	ttgataaagctatgattctcgttatgtctgtctattttagctataactaaattttgt	1303
Db	1217	TTTGAAATTTGGTTTTCGATGCCCGTTATCTTCCGAAATTTACAAATATATGAAATTTCTTAC	1276
QY	1304	ctggcctcaaatgaagatgtgaagccggaacgcttatgtcaatccacccaacagctgttg	1363
Db	1277	TGACTTTAAACAAAGAATTTCAGCAGAAACGTCTCATCCCTATTTTACTCAGCAGCAATGCG	1336
QY	1364	atataatatttgttgatgttagcaggtatataccaatttgggttgaaacgcatlaagacggaa	1423
Db	1337	ATAACCAATTTGGTATTATTAGCTGTGATTATAGCCGTATTAGGTAAAAAGTCCTTATGTGTA	1396
QY	1424	aagcttatgaagatgtcttttgaagaatgggaagaagaattgaagctgtgtccaatattact	1483
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QY	1484	tgaatgtctaaactggtatcatagacatgaattgaattcaaatgggaaaaaacgcgaacgct	1543
Db	1457	TGGAATTGGCAAAACGGATATTATTGATGTGATGATTTGCGGTTAAACGAAACATCAGCAT	1516
QY	1544	tgcatttcaacttcgctttgtttaaagcaggaactgaaatcaagttgaacggtttaactatg	1603
Db	1517	TCTTATTTCAGAACCCATTATTATACGCCCGGGAACACAGCATGCTAAGCGCTGAACAAACAG	1576
QY	1604	gtaaatactctatataatgaatgaatctgaagatgttaaaaaacgtgcgaagttaag	1663
Db	1577	GTAATATTGAATATTATTACCAACCTCAATATTAAACCGTTAATAGCTGGAATAATTACAG	1636
QY	1664	atggaagagctagttctaaattagatttctctaaagtatccaaggtatccaagctgtgacgaagacg	1723
Db	1637	ATGTGTGACGAAGATTCTTACCTTTGATTATTAACTAACCTGTTACAGCGTATTGGTATTGAAT	1696
QY	1724	aaggcacagacagagattggtctctaagttaagtcaaaa-----g	1762
Db	1697	TAGACAAATGCTGGAAATGTAACTTAATAAACCAACAAACAAATAATTATTGCCAAACTTGGTG	1756
QY	1763	cttgcgaatgacagatatcttctgtgtcgaagttaaaatgtaatatgtatggttggaaatggac	1822
Db	1757	AAGTGATGATCAACAGTATTTTGTTGGTTCTGTGTCACGAGGAATGATGGCGGTGAAGGTTT	1816
QY	1823	acgagtgtctctctataagtaaaagcaggaattgtgtatatactgtatagatgtga	1882
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QY	1943	atgaagctgttgaagcgctcaagaacccaaggtggtgtaaacgtaactgaactacagiatc	2002
Db	1934	ACGAAGTGACTTCAACCCCATTAACCGATTAGTGGCGCAACCGTGAAGAAAAAATTAGATATATC	1993
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QY	2063	tagaagaagtaattgttctcgaatttaagtatctcaagaagttcctaattcaacagaca	2122
Db	2051	TTGAGGAATTAATTCGGTACATCACCATTACGATATCTTTAAAGTAGTAAAGTTCAATGATG	2110
QY	2123	tattccatagttgtgaaggtgatgtatttaactcogatbgttgtgtcgtgtgaacccgcttgc	2182
Db	2111	CCTTTAACGGTGTGATGGTGTGCTGCTACTATTATGACGGGTACACGCGGCATATCCGCTTAT	2170
QY	2183	tttgtgtgaagaagcaacgatcgcacttcttgtagatgaagcgatgattactgattgagcg	2242
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LOCUS	BD009870		
DEFINITION	GHRH-leukotoxin chimera.		
ACCESSION	BD009870		
VERSION	BD009870.1 GI:18638243		
KEYWORDS	JP 2001502887-A/3.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 2794)		
AUTHORS	Potter,A.A. and Manns,J.G.		
TITLE	GHRH-leukotoxin chimera		
JOURNAL	Patent: JP 2001502887-A 3 06-MAR-2001;		
COMMENT	UNIVERSITY OF SASKATCHEWAN		
	OS Unidentified		
	PN JP 2001502887-A/3		
	PD 06-MAR-2001		
	PF 08-AUG-1997 JP 1998509192		
	PR 09-AUG-1996 US 08/694865		
	PI ANDREW A POTTER, JOHN G MANN		
	PC C12N15/16, C12N15/31, C12N15/62, C12N1/21, C07K14/285, C07K7/23, PC		
	A61K38/09,		
	PC A61K39/385		

CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 1..2778.
source 1..2794
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BASE COUNT 930 a 487 c 599 g 778 t
ORIGIN

Query Match 29.3%; Score 814.4; DB 6; Length 2794;
Best Local Similarity 60.2%; Pred. No. 6.2e-133;
Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

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DB 29 CAAAACCTGGGCGNAAAAAATATCTCTATATTCCTCCCAAAATATACCAATATGATCTG 88
QY 107 aaaaagctgggactttaagattttaaaagctgctgataagattgattgctcgtc 166
DB 89 AACAGGTAATGTTTACAGATTATCTCAAAAGCGCCGAAGATTGGGATTTAGGTAC 148
QY 167 taagcagaagccctaacacactgaacaagaacaaatcgtgtgacacagtaaacagt 226
DB 149 AAAGAGAAAGAACGCAATATATTTGCAACAGCTCAACACAGTTTACGACAGATTCAACCG 208
QY 227 tctctctccacaacaaactgtaactgctatcttgcaacaaatagaaaagctctac 286
DB 209 CTATTGGCTTAACGACGCTGGCATTTGTATTCCTCCCAAAATTTGATTAATTTGCTAC 268
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DB 269 AGAAA-----ACTAAAGCAGCGCAACGATTAGTTCTGCGGAAAGCATTTGTACAAA 319
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DB 320 ATGCAATTAAGCCAAACACTGATTTATCTGCAATTCATCTATTTTATTTAGGCTCACTATTTGG 379
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DB 380 CTGGAATGATTTAGATGAGAGCCTTACAGAA--TAACAGAACCAACATGCTCTTGCTA 436
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QY 527 ttgaagcatttcttcaagttagcaagttaggttactactatctgcaagctaaagct 586
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RESULT 13
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DEFINITION Sequence 1 from patent US 5534256.
ACCESSION 123447
VERSION 123447.1 GI:1603317
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2794)
AUTHORS Potter, A.A. and Harland, R.J.
TITLE Haemophilus somnus outer membrane protein extract enriched with iron-regulated proteins
JOURNAL Patent: US 5534256-A 1 09-JUL-1996;
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BASE COUNT 930 a 487 c 599 g 778 t
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Best Local Similarity 60.2%; Pired. No. 6; 2e-133;
Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

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Db 677 ATGCTTCAACAGCTTAAAAAGTGGGTGGGCTTTTGAATTTGGCAAAACCAAGTTGTTGTA 736
Qy 764 atgtaacaaaagcaatttctcataitgtttaagacaacgltgtcgtcgtgctalcaa 823
Db 737 ATATTACCAAAAGCGCTTCTTCTTACATTTTAGCCCAACGTTGACAGAGTTATCTT 796
Qy 824 ctactgtgctgttgcgtcttaacttactcactgatagttgcaattagtccttgg 883
Db 797 CAACGTGGCCCTGCTGCTTAAATTCCTTACTGTTTCTCTTGCAATGGCCCATTAAG 856
Qy 884 cattatgaatgcaagataaactcaactcaactgctaaigtctcgtgaaglttgcaaac 943
Db 857 CATTTGCCGATATGCGGATTAATTTAATCTGCAAAAAGTTTGAAGGTTATGCCGAAAC 916
Qy 944 aattccgaanaatttggctatgataggggatcatltatggtgaaatcagcgylgtg 1003
Db 917 GCTTAAAAAATTTAGGCTATGACGAGATATTTATTAGCAAAATATCAGGGGGAACAG 976
Qy 1004 gtactatgaaagcttcaactaactaacttagtagcgaacttagtgcaggttctcgtg 1063
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Qy 1064 ttccgctgctgctgtagaactcgtcgtlgtgtgacgcagatgacactatgttcaggtg 1123
Db 1037 TGTCTGCTGCTGACGCCGCGCTCGGTTATTGCTTCAACGATTCGCTTATTACTGCGGA 1096
Qy 1124 ttacagatctgactcgtgaaattttaagaacgltcaacaggtcaatgttggaaagtgtg 1183
Db 1097 TTACCGGTGTAATTTCTACGATTTTCGCAATTTCTTAAACAAGCAATGTTTAGCAGCGTTG 1156
Qy 1184 ctaacgctttcaagaagttaaaattttaagagtggaaaagcaaaatggtgcgtgaactat 1243
Db 1157 CAAAATAAATTCATATACAAAATTTGTAATGGAATGGAAAAAATATATACGCTATGAACTCT 1216
Qy 1244 ttgataaaggctatgacttcgtgtaigtgtctatcttagcctaataactaaatlttgt 1303
Db 1217 TTGAAAAATGGTTAGCATGCCGCTTATCTTGGCAATTTTCAAGATTAATTAAGAAATCTTAC 1276
Qy 1304 ctgagctaataaagaagtggaaagctgaaacgtgtatattgcaatcaccacaacagttgg 1363
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Db 1337 ATTAACAACCTTGGTATTTAGCTGTGATTAAGCCGTTTAGGTAAAAAAGTCTTAAAGTGA 1396
Qy 1424 aagctatgcaagatccttttgagaatggtgcaagaagaagtggaaagctggttccaatlactt 1483
Db 1397 AAGCCTATGTGATGCTGTTTGAAGAAGCAAAACACATTAAACCCATTAATTAAGTACAGT 1456
Qy 1484 tggatgtctaaacgtgtatcatagacatagttaattcaaatgggaaaaaaagcaagcgt 1543

Db 1457 TGGATTCGGCAAAACGGTATTATTTGATGTGAGTAATTCGGGTAAAGCAAACTCAGATA 1516
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Db 1517 TCTTATTACGAAGGCCATTAATTGACGCCGGGAACAGAGATGCTGTAACCCGTAACAAACG 1576
Qy 1604 gtaataactcttatataaaglttaaaatcggagcgtgtgtaaaaaatggtgcaagttacag 1663
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Qy 1883 gtcaacagaagaacgacgtatatacagttaaactgtaaggtgttcgaggtatatactaac 1942
Db 1874 AAGAGACCGAGCAAGAGTAGTATATACCGTAATATGTTTGTGTAAGAACCGTAAGCACTAC 1933
Qy 1943 atgaagttgtgaagcgttcaagaacaaaggtgggttaacgtactgnaaactatccaglac 2002
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Qy 2003 gtgattatgaattaagaanaagttggtatgtgtatcgaactcagctaacgataatttgaatcag 2062
Db 1994 GTCTATTACCAATTAACACGACCATTG---CCGTTATTATACCAAAAGTACTGTAAGGCTG 2050
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Qy 2123 tatccaatgtgtgtgaaggtgatatctactcgaatgtgtgtcgtggtggaagcagcgtgt 2182
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Qy 2183 ttgtgtgtaagaagcaacgatcgaacttctgagatgtaaggtcgaatlttaactgatlgtgcg 2242
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Qy 2423 atcatcaggtagatlaaacaalacagaatgtgtcatataacataacttaacaaa----- 2477
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Db 2528 AOCGATCACCTCAAAAGCAAGTTGATGATCTTAT 2561

LOCUS	180029	14	180029	2794 bp	DNA	linear	PAT 10-JUN-1998
DEFINITION	Sequence	1	from patent	US 5708155.			
ACCESSION	180029						
VERSION	180029.1		GI:3208319				
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 2794)						
AUTHORS	Potter, A.A., Redmond, M.J. and Hughes, H.P.A.						
TITLE	Enhanced immunogenicity using leukotoxin chimeras						
JOURNAL	Patent: US 5708155-A 1.13-JAN-1998;						
FEATURES	Location/Qualifiers						
source	1..2794		/organism="unknown"				
BASE COUNT	930 a	487 c	599 g	778 t			
ORIGIN							
Query Match	29.3%	Score 814.4;	DB: 6;	Length 2794;			
Best Local Similarity	60.2%	Pred. No. 6.2e-133;					
Matches 1538;	Conservative	0;	Mismatches 956;	Indels 60;	Gaps		
Qy	53	caaaagctcgtatgaataaatcttctactcgtcgtatcccaagaat-----tatgaccgc	106				
Db	29	CAAAACCTGGGGGCAAAAAATATATCCCTATATTCGCCCAAAATACCAATATGATGACTCG	88				
Qy	107	aaaaagctggagactttaaagcttattaaagctgcgtatgaattagatttgcgtc	166				
Db	89	AACAGAGTAAAGGCTTTACAGATTATAGCAAAAGCGCGCGAAGAGCTGGGATTTGAGGTAC	148				
Qy	167	tagaagaagagccttaatacactgaacgaacaaaaaactcgttgcacagtaaatcagc	226				
Db	149	AAAGAGAAAGAACGCATATATATTTGCACACAGCTCAACACAGTTTACGACGATTCACACCG	208				
Qy	227	tctctctctcacaaactgtagtcttcttctctcgcacaaatagaataaagttctac	286				
Db	209	CTATGCGCTTAACGTAGAGCGGTGGCATTTGTTATCCGCTCCACAAATGTATTAATGGCTAC	268				
Qy	287	aaaaacattctcaacataagcttagcccaaggttagaacaagtgtagaataaatatgtagc	346				
Db	269	AGAAA-----ACTTAAACGAGGCCAAGCATTAAGTTCTGCCGAAAGCATTTGACAAA	319				
Qy	347	aattaggaagaagtaagtattatcatcaacatbaagctcttttgggcaactgtag	406				
Db	320	ATGCAAATTAAGCCAAACCTGATTTATCTGGCATTTCATCTATTTTACGCTCAGATTTGG	379				
Qy	407	cgggtatagaacttgaatcttctaacaacaaaagtgatgcgtgcacgtatgcttgcta	466				
Db	380	CTGGATATGATTTAGTATAGCGCTTACGAA---TAAACAGAACCCAAACATGCTCTTGCTA	436				
Qy	467	aagcctagatgaacttgaatgaagataattgtgaactctctcgaaggtactcaaaaga	526				
Db	437	AAAGCTGGCTTGAGAGCTAACAAATTCATTAATTTGAATAATTTGCTTAATTCAGTAAACAC	496				
Qy	527	ctgaagcaattctctcacagcttagcaaaagttagtcttcaactatacgcgaagctaaagct	586				
Db	497	TTGACGATTTGGTGTAGCAAAATTAATGCTCAATTTGGTTCAAAACTACAAATATCAAAAGCT	556				
Qy	587	tctctcaatataggaaacaagctgtcaaaactcaat---tttctcaaacaaactctggtc	643				
Db	557	TAGGAGCTTTTAGGAGCAAACTCAAAATTAATTCGGTGAAGCTGATTAACCTGGCCTTGGT	616				
Qy	644	tggaataataactactggttctgctatacaggaactttcgcagcgttctgcttagcgataaaa	703				
Db	617	TAGATGTTATCTCAAGGGCTATTATTCGGGCGCAACAGCTGCACCTTGTACTTGACAGTTAAA	676				
Qy	704	atgcaatgcactggcaaaaagattgctgcaggttttgaataagcaatcaagatttggta	763				

Db	677	ATGCTTCAACAGCTAAANAAGGGGTGGGGGTTTGAATTTGGCAACCAAGTGTGGTA	736
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Db	737	ATATTACCAAGCCGTTTCTTCTTACATTTTAAAGCCCAAGGTGTACAGCTTATCTT	796
Qy	824	ctactggtgctgttgcgtcttataacttaactcgaataatglttgcaattgctcttgcg	883
Db	797	CAACGGGCGTGTGGCTCTTTAATTTGGTTCTACGTTTCTCTTGGATTTAGCCCATTAAG	856
Qy	944	aattccgaanaatttgcgtcatgatvggagacatctatctgctgaataatcagcgtgtgtgcg	1003
Db	917	GCTTTAAAAAATTAGCTATGACGGAGATTAATTTATTTAGCAGAAATATCAGCGGGAGACAG	976
Qy	1004	gtactatctgaagcttcatctaaactaaatagtacggcattaggtgcagttctctgtgtg	1063
Db	977	GGACATTATGATGCACACGGGTACTGTGAATTTAATCCGACATTTGGCCCTATTTGCTGGTGGTG	1036
Qy	1084	tttcgcgtgcgtcgttgaagatcgtctgtgttgagacagattpcaacttaagtctgagatg	1123
Db	1037	TGTCTGCTGCTGCACAGCCGGCTCGTTATTGCTTCAACCATTCCTTATTAGTATCTGGGA	1096
Qy	1124	ttacaggaattgactctcgtgaatttttagaagcgtctcaaacagggcaatgtttgaaagtgtg	1183
Db	1097	TTACCGGTGTAAATTTCTACGATTTGCAATTTTCGAATTTTAAACAAGCAATGTTTGACGACGTGG	1156
Qy	1184	ctaacgctttacaaggtataaattttagagttvggaaagcaaaatgvcggttcagaactatc	1243
Db	1157	CAAAATMAATTCATACCAAAATTGTAGATGATGGAAAAAATATATCCGTAAAGAACTACT	1216
Qy	1244	ttgataaaggctatgattctcgtttatgctgtctatttagcctaactaaatttttgt	1303
Db	1217	TTGAATAAGGTATGACATGCCCGCTTATCTTGGCAATTTACAGATATATTTGAATATCTTAC	1276
Qy	1304	ctgagctaaataaagttctgagacgtctgaacgtgtctattctgcaalccaaccaacaagcttgg	1363
Db	1277	TGAATTTAACAACAAGTTTACAGCGACAAAGTGTATGCTATTTCTCAGCGACGAATGGG	1336
Qy	1364	ataataataatcggvtgagtttagcaggltatccaatatcgggtgagacgcattlaagagcggaa	1423
Db	1337	ATAACAAATTTGATTTAGCTGTATTAGCGCTTATAGTGGTGAATAAAGTCCCTACTCGGTA	1396
Qy	1424	aagctatgcagatgctcttttagaagttgccaagaagaagttgaagctgtgtlccaatatctt	1483
Db	1397	AAGCCTATGTGTGATCGTTTGAAGAAGCCAAACACATTTAAACCCCATTAATTTAGTACAGT	1456
Qy	1484	tgaagctcaaaaactgtatcatagacatagttaattccaatttvggaaaaaagcagaagcgt	1543
Db	1457	TGGATTTCCGCAAAAGCGTATTATTATTTGATGTGTAGTAATTTCCGGTTAAACGAAACCTCAGCATTA	1516
Qy	1544	tgcaattcaactcgcctttgtttaacagcaggaactgaatcagcgtgaacgcttataacta	1603
Db	1517	TCTTATTCAGAAAGCCGCAATTTATGTAGCCGGGACACAGACATCTGTGAAGCGTACAAACAG	1576
Qy	1604	gtaataactctatataatgaataagttaaatctgcgcgtgttaaaaaacatgcgcgaagtctag	1663
Db	1577	GTAATTTATGAATATTTTATTTACCAAGCTCAATATTAAACCGTGTATATGTGTGGAATAATTACAG	1636
Qy	1664	atgagagagctagttcttaataatagattctctcaaaagtatacgaagtgtlagccgagacag	1723
Db	1637	ATGTGTCAGACGAAGTTCTTACCTTTTATTTATTTACTTAACAGTGTCTTACAGCTATTTGGTATTTGAAT	1696
Qy	1724	aagcagacagacgagatlgltcttaataagttaaatgcaaaa-----g	1762
Db	1697	TAGACAAATGCTGGAATATGTAACATAAACAAGAAAGAAATAATTTATTCGCAAACTTGGTG	1756
Qy	1763	ctgagcaatgacgatactcttgtgtgttgcataaggtataaaatgaaatatgaaatgtgtgagatgac	1822
Db	1757	AAGGTATGACAAACCTATTTTGTGTGTCTGTGTACACAGCAAAATTTATGTGGCTGTGAAGTTT	1816

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 09:01:25 ; Search time 65.81 Seconds

(without alignments)
31.544 Million cell updates/sec

Title: US-09-884-696-6
Perfect score: 57
Sequence: 1 FLSLNKLEAE 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	927	2 Q93G12	Q93G12 moraxella b
2	43	75.4	946	2 Q9EV24	Q9EV24 mannheimia
3	43	75.4	953	2 Q9ETX2	Q9ETX2 mannheimia
4	43	75.4	953	2 Q9ETG5	Q9ETG5 pasteurella
5	43	75.4	953	2 Q9EV34	Q9EV34 pasteurella
6	43	75.4	953	2 Q9EV33	Q9EV33 pasteurella
7	43	75.4	953	2 Q9EV32	Q9EV32 pasteurella
8	43	75.4	953	2 Q9EV31	Q9EV31 pasteurella
9	43	75.4	953	2 Q9EV30	Q9EV30 pasteurella
10	43	75.4	953	2 Q9EV29	Q9EV29 pasteurella
11	43	75.4	953	2 Q9EV27	Q9EV27 pasteurella
12	43	75.4	953	2 Q9EV26	Q9EV26 mannheimia
13	43	75.4	953	2 Q9EV25	Q9EV25 mannheimia
14	43	75.4	953	2 Q9EV23	Q9EV23 mannheimia
15	43	75.4	953	2 Q9EV28	Q9EV28 pasteurella
16	43	75.4	954	2 Q9EUE1	Q9EUE1 pasteurella

17	43	75.4	955	2 Q9EUD4	Q9EUD4 pasteurella
18	43	75.4	955	2 Q9EV22	Q9EV22 pasteurella
19	43	75.4	956	2 Q93NP1	Q93NP1 actinobacill
20	42	73.7	897	13 Q13098	Q13098 xenopus lae
21	42	73.7	913	13 Q13099	Q13099 xenopus lae
22	39	68.4	798	13 Q90307	Q90307 carassius a
23	38	66.7	73	9 Q9MBS7	Q9MBS7 staphylococ
24	38	66.7	73	9 Q9G032	Q9G032 bacterioph
25	38	66.7	73	16 Q932B3	Q932B3 staphylococ
26	38	66.7	211	9 Q80148	Q80148 bacterioph
27	38	66.7	222	5 Q9V3V7	Q9V3V7 drosophila
28	38	66.7	382	16 Q25891	Q25891 helicobacte
29	38	66.7	508	5 Q18051	Q18051 caenorhabd
30	38	66.7	977	4 Q75300	Q75300 homo sapien
31	38	66.7	977	4 Q9H476	Q9H476 homo sapien
32	38	66.7	993	2 Q52054	Q52054 enterococc
33	38	66.7	1407	4 Q96S82	Q96S82 homo sapien
34	38	66.7	1586	4 Q9P2E9	Q9P2E9 homo sapien
35	37	64.9	275	11 Q63306	Q63306 rattus norv
36	37	64.9	646	11 Q63779	Q63779 rattus norv
37	37	64.9	653	2 Q9RJU0	Q9RJU0 streptomyce
38	37	64.9	899	10 Q9C895	Q9C895 arbidopsi
39	37	64.9	913	11 Q9QYX7	Q9QYX7 cricetus
40	37	64.9	1300	11 P97692	P97692 rattus norv
41	37	64.9	1534	6 Q28298	Q28298 canis famil
42	37	64.9	2779	5 Q9W4N7	Q9W4N7 drosophila
43	36	63.2	117	10 Q80380	Q80380 daucus caro
44	36	63.2	141	11 Q88651	Q88651 marmota mon
45	36	63.2	151	10 Q04767	Q04767 bolusanthus

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	927 AA.
Q93G12	Q93G12	Q93G12		
AC	Q93G12	Q93G12		
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	RTX TOXIN.			
GN	MBXA.			
OS	Moraxella bovis.			
OC	Bacteria: Proteobacteria: gamma subdivision: Moraxellaceae: Moraxella.			
OX	NCBI_TaxID=476;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-TIFON I;			
RX	MEDLINE-21388402: PubMed-11497442;			
RA	Angelos J.A., Hess J.F., George L.W.;			
RT	"Cloning and characterization of a Moraxella bovis cytotoxin gene.";			
RL	Am. J. Vet. Res. 62:1222-1228(2001).			
DR	EMBL: AF205359; AAK84651.1; "			
SO	SEQUENCE 927 AA; 98845 MW; F4B703577E10A96D CRC64;			
Query Match	100.0%;	Score 57;	DB 2;	Length 927;
Best Local Similarity	100.0%;	Pred. No. 0.17;		
Matches 12;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1 FLSLNKLEAE 12			
DB	433 FLSLNKLEAE 444			
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ID	Q9EV24	PRELIMINARY;	PRT;	946 AA.
AC	Q9EV24;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			

DE LEUKOTOXIN.
 GN LKTA.
 OS Mannheimia glucosida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=85401;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH574;
 RX MEDLINE=21101823; PubMed=11157953;
 RA Davies R.L., Whitlam T.S., Selander R.K.;
 RT "Sequence Diversity and Molecular Evolution of the leukotoxin (lktA)
 RT gene in bovine and ovine strains of Mannheimia (pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 183:1394-1404(2001).
 DR EMBL; AF314521; AAC40305.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrtse.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam: PF003353; hemolysincabind; 1.
 DR Pfam: PF02382; RTX; 1.
 DR PRINTS; PR00313; CABNDNGRPT.
 DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
 SQ SEQUENCE 946 AA; 101480 MW; 25C07858BDC76C4 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 946;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
 Db 444 FLNLNKELOAE 455

RESULT 3
 Q9ETX2 PRELIMINARY; PRT; 953 AA.
 AC Q9ETX2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Mannheimia glucosida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=85401;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH498, AND PH344;
 RA Davies R.L., Whitlam T.S., Selander R.K.;
 RT "Sequence diversity and molecular evolution of the leukotoxin (lktA)
 RT gene in bovine and ovine strains of Mannheimia (pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 0:0-0(2001).
 DR EMBL; AF314518; AAC40302.1; -;
 DR EMBL; AF314517; AAC40301.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrtse.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam: PF003353; hemolysincabind; 1.
 DR Pfam: PF02382; RTX; 1.
 DR PRINTS; PR00313; CABNDNGRPT.
 DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
 SQ SEQUENCE 953 AA; 102135 MW; 70DB354157F5881E CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12

Db 451 FLNLNKELOAE 462
 RESULT 4
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 AC Q9ETG5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH284, PH388, AND PH8;
 RA Davies R.L., Whitlam T.S., Selander R.K.;
 RT "Sequence diversity and molecular evolution of the leukotoxin (lktA)
 RT gene in bovine and ovine strains of Mannheimia (pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 0:0-0(2001).
 DR EMBL; AF314507; AAC40291.1; -;
 DR EMBL; AF314504; AAC40288.1; -;
 DR EMBL; AF314506; AAC40290.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrtse.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam: PF003353; hemolysincabind; 1.
 DR Pfam: PF02382; RTX; 1.
 DR PRINTS; PR00313; CABNDNGRPT.
 DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
 SQ SEQUENCE 953 AA; 101997 MW; D593D6A577C3ADE9 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
 Db 451 FLNLNKELOAE 462

RESULT 5
 Q9EV34 PRELIMINARY; PRT; 953 AA.
 AC Q9EV34;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH56;
 RX MEDLINE=21101823; PubMed=11157953;
 RA Davies R.L., Whitlam T.S., Selander R.K.;
 RT "Sequence Diversity and Molecular Evolution of the leukotoxin (lktA)
 RT gene in bovine and ovine strains of Mannheimia (pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 183:1394-1404(2001).
 DR EMBL; AF314505; AAC40289.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrtse.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.

DR Pfam: PF00353; hemolysincabind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102010 MW; DE48B28E0E0B09FB CRC64;

Query Match
Best Local Similarity 75.4%; Score 43; DB 2; Length 953;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
|| |||||:|

Db 451 FLTLNKELEQAE 462

RESULT 6

O9EV33 PRELIMINARY; PRT; 953 AA.

AC O9EV33:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE LEUKOTOXIN.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PH66;
RX MEDLINE=21101823; PubMed=1157953;
RA Davies R.L., Whitlam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica."
RL J. Bacteriol. 183:1394-1404(2001).
RL EMBL: AF314508; ANG40292.1; -;
DR InterPro: IPR001753; Enoyl_COA_hydrtse.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysincabind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102132 MW; 4138AB5FAE2843B3 CRC64;

Query Match
Best Local Similarity 75.4%; Score 43; DB 2; Length 953;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
|| |||||:|

Db 451 FLTLNKELEQAE 462

RESULT 7

O9EV32 PRELIMINARY; PRT; 953 AA.

AC O9EV32:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-PH706;
RX MEDLINE=21101823; PubMed=1157953;
RA Davies R.L., Whitlam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica."
RL J. Bacteriol. 183:1394-1404(2001).
RL EMBL: AF314509; ANG40293.1; -;
DR InterPro: IPR001753; Enoyl_COA_hydrtse.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysincabind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102078 MW; EF425243C8741BE4 CRC64;

Query Match
Best Local Similarity 75.4%; Score 43; DB 2; Length 953;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
|| |||||:|

Db 451 FLTLNKELEQAE 462

RESULT 8

O9EV31 PRELIMINARY; PRT; 953 AA.

AC O9EV31:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PH588;
RX MEDLINE=21101823; PubMed=1157953;
RA Davies R.L., Whitlam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica."
RL J. Bacteriol. 183:1394-1404(2001).
RL EMBL: AF314510; ANG40294.1; -;
DR InterPro: IPR001753; Enoyl_COA_hydrtse.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysincabind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102160 MW; A189BF80754A7907 CRC64;

Query Match
Best Local Similarity 75.4%; Score 43; DB 2; Length 953;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
|| |||||:|

Db 451 FLTLNKELEQAE 462

RESULT 9

O9EV30 PRELIMINARY; PRT; 953 AA.

AC O9EV30:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.

DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH196;
 RX MEDLINE=21101823; PubMed=11157953;
 RA Davies R.L., Whittam T.S., Selander R.K.;
 RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
 RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 183:1394-1404(2001).
 DR EMBL: AF314512; AAC40296.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrtse.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003353; RTX_N.
 DR Pfam: PF003353; hemolysincabind; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1
 SQ SEQUENCE 953 AA; 102043 MW; 4E8F11490479A69A CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLSELNKELEAE 12
 || |||||:
 Db 451 FLNLNKELEAE 462

RESULT 10
 Q9EV29 PRELIMINARY; PRT; 953 AA.
 AC Q9EV29;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH278;
 RX MEDLINE=21101823; PubMed=11157953;
 RA Davies R.L., Whittam T.S., Selander R.K.;
 RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
 RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 183:1394-1404(2001).
 DR EMBL: AF314514; AAC40298.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrtse.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003353; RTX_N.
 DR Pfam: PF003353; hemolysincabind; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1
 SQ SEQUENCE 953 AA; 102147 MW; 11600FDA7849A1CA CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
 Best Local Similarity 75.0%; Pred. No. 45;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 FLSELNKELEAE 12
 || |||||:
 Db 451 FLNLNKELEAE 462

RESULT 11
 Q9EV27 PRELIMINARY; PRT; 953 AA.
 AC Q9EV27;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH392;
 RX MEDLINE=21101823; PubMed=11157953;
 RA Davies R.L., Whittam T.S., Selander R.K.;
 RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
 RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 183:1394-1404(2001).
 DR EMBL: AF314516; AAC40300.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrtse.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003353; RTX_N.
 DR Pfam: PF003353; hemolysincabind; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1
 SQ SEQUENCE 953 AA; 102230 MW; 2B686808EB370090 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLSELNKELEAE 12
 || |||||:
 Db 451 FLNLNKELEAE 462

RESULT 12
 Q9EV26 PRELIMINARY; PRT; 953 AA.
 AC Q9EV26;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Mannheimia glucosida.
 OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=85401;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH240;
 RX MEDLINE=21101823; PubMed=11157953;
 RA Davies R.L., Whittam T.S., Selander R.K.;
 RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
 RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 183:1394-1404(2001).
 DR EMBL: AF314519; AAC40303.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrtse.

DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PR00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102236 MW; AC5874B3B75D1C98 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
DB 451 FLNLNKELOAE 462

RESULT 13

O9EV25 PRELIMINARY; PRT; 953 AA.
AC O9EV25;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OS Mannheimia glucosida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=85401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PH496;
RX MEDLINE-21101823; PubMed-11157953;
RA Davies R.L., Whittam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica";
RL J. Bacteriol. 183:1394-1404(2001).
DR EMBL: AF314520; AAG40304.1; -;
DR InterPro: IPR001753; Enoyl_CoA_hydrase.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PR00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102138 MW; CA1D9EBC1D799951 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
DB 451 FLNLNKELOAE 462

RESULT 14

O9EV23 PRELIMINARY; PRT; 953 AA.
AC O9EV23;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OS Mannheimia glucosida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=85401;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PH290;
RX MEDLINE-21101823; PubMed-11157953;
RA Davies R.L., Whittam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica";
RL J. Bacteriol. 183:1394-1404(2001).
DR EMBL: AF314522; AAG40306.1; -;
DR InterPro: IPR001753; Enoyl_CoA_hydrase.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PR00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102150 MW; D99C36DA595B1624 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
DB 451 FLNLNKELOAE 462

RESULT 15

O9EV28 PRELIMINARY; PRT; 953 AA.
AC O9EV28;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEUKOTOXIN (LKTA).
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PH292, AND PH296;
RX MEDLINE-21101823; PubMed-11157953;
RA Davies R.L., Whittam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica";
RL J. Bacteriol. 183:1394-1404(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PH296;
RA Davies R.L., Campbell S., Whittam T.S.;
RT "Mosaic structure and molecular evolution of the leukotoxin operon
RT (lktCABD) of Mannheimia (pasteurella) haemolytica, Mannheimia
RT glucosida and Pasteurella trehalosi";
RL J. Bacteriol. 0:0-0(2001).
DR EMBL: AF314515; AAG40299.1; -;
DR EMBL: AF414141; AAL13281.1; -;
DR InterPro: IPR001753; Enoyl_CoA_hydrase.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PR00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102218 MW; 04AB1715B819E571 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
Best Local Similarity 75.0%; Pred. No. 45;

Matches	9;	Conservative	1;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	FLSEINKELAE	12						
Db	451	FLNINKELQAE	462						

Search completed: September 11, 2002, 09:01:26
Job time: 284 sec

ALIGNMENTS

RESULT 1
 AAF57290
 ID AAF57290 standard; DNA: 3231 BP.
 XX AAF57290;
 AC
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE M. bovis Dalton 2d RTX toxin A subunit encoding DNA.
 XX
 KW Moraxella; antigen; immune response; infection; RTX toxin; vaccine;
 KW antibacterial; ds.
 XX
 OS Moraxella bovis.
 XX
 EH location/Qualifiers
 FT 232..3015
 FT /tag- a
 FT /product- "RTX toxin A subunit"
 FT 1..195
 FT /tag- b
 FT /note- "partial coding region of RTX toxin C subunit"
 FT 3080..3250
 FT /tag- c
 FT /note- "partial coding region of RTX toxin B subunit"
 CDS
 CDS
 CDS
 XX
 XX
 PN WO200116172-A1.
 XX
 PD 08-MAR-2001.
 XX
 PF 31-AUG-2000; 2000WC-AU01048.
 XX

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68217

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RESULT 1
AAB62110
ID AAB62110 standard: Protein: 927 AA.
XX
AC AAB62110:
XX
DT 29-MAY-2001 (first entry)
XX
DE M. bovis Dalton 2d RTX toxin A subunit.
XX
KW Moraxella: antigen; immune response; infection; RTX toxin; vaccine;
XX antibacterial; A subunit.
XX
OS Moraxella bovis.
XX
EN MO200116172-A1.
XX
PD 08-MAR-2001.
XX
PF 31-AUG-2000; 2000MO-AU01048.
XX
PR 31-AUG-1999; 99AU-0002571.
XX
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX (UYME ) UNIV MELBOURNE.
XX
PI Farn J, Strugnelli R, Tennent J;
XX
XX WPI: 2001-235092/24.
XX DR N-PSDB: AAF57290.
XX
XX Novel Moraxella bovis antigen useful in compositions for raising immune
XX response in an animal, has protease, lipase or hemolysin activity
XX
PS Claim 26: Fig 5; 60pp; English.
XX
XX The invention relates to new Moraxella bovis antigens and nucleic acid
XX sequences encoding these antigenic polypeptides. The antigenic
XX polypeptides and polynucleotides are useful for raising an immune
XX response in an animal directed against Moraxella, preferably against
XX M. bovis or M. catarrhalis, and for treating Moraxella infections. The
XX present sequence represents the amino acid sequence of the A subunit of
XX the RTX toxin from M. bovis Dalton 2d.
XX
XX Sequence 927 AA:
XX
SO

```

Query Match 100.0%; Score 77; DB 22; Length 927;
 Best Local Similarity 100.0%; Pred. No. 7,4e-05; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0;
 OY 1 FNDIFHSGECDLL 14
 Db 705 fndifhsgegdll 718

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ALIGNMENTS

SEQ 6

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RESULT 1
AAB62110
ID AAB62110 standard; Protein; 927 AA.
XX
AC AAB62110;
XX
DT 29-MAY-2001 (first entry)
XX
DE M. bovis Dalton 2d RTX toxin A subunit.
XX
KW Moraxella; antigen; immune response; infection; RTX toxin;
KW antibacterial; A subunit.
XX
OS Moraxella bovis.
XX
PN WO200116172-A1.
XX
PD 08-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-AU01048.
XX
PR 31-AUG-1999; 99AU-0002571.
XX
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA (UYME ) UNIV MELBOURNE.
XX
PI Farn J, Strugnell R, Tennent J;
XX
DR WPI; 2001-235092/24.
DR N-PSDB; AAF57290.
XX
PT Novel Moraxella bovis antigen useful in compositions for raising immune
PT response in an animal, has protease, lipase or hemolysin activity
XX

```

PS Claim 26; Fig 5; 60pp; English.

XX
 CC The invention relates to new Moraxella bovis antigens and nucleic acid
 CC sequences encoding these antigenic polypeptides. The antigenic
 CC polypeptides and polynucleotides are useful for raising an immune
 CC response in an animal directed against Moraxella, preferably against
 CC M. bovis or M. catarrhalis, and for treating Moraxella infections. The
 CC present sequence represents the amino acid sequence of the A subunit of
 CC the RTX toxin from M. bovis Dalton 2d.
 XX
 SQ Sequence 927 AA;

Query Match 100.0%; Score 57; DB 22; Length 927;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FLSELNKELEAE 12
 |||||
 Db 433 flselnkeleae 444

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530 13

RESULT 5
 AAR86998
 ID AAR86998 standard; Protein; 758 AA.
 XX
 AC AAR86998;
 XX
 DT 04-JUL-1996 (first entry)
 XX
 DE Enterohaemorrhagic E.coli hlyA gene product.
 XX
 KW Enterohaemorrhagic Escherichia coli; virulent; EHEC; O157:H7 serotype;
 KW detection; probe; primer; hlyA gene; enterohaemorrhagic colitis;
 KW haemolytic uremic syndrome; mesenteric adenitis.
 XX
 OS Escherichia coli (enterohaemorrhagic).
 XX
 PN US5475098-A.
 XX
 PD 12-DEC-1995.
 XX
 PF 14-JUN-1994; 94US-0258188.
 XX
 PR 14-JUN-1994; 94US-0258188.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Hall RH, Xu JG;
 XX
 DR WPI; 1996-048546/05.
 DR N-PSDB; AAT08098.
 XX
 PT Enterohaemorrhagic E. coli (EHEC) nucleic acid sequences - useful
 PT for probe and primer design for sensitive and specific detection of
 PT EHEC
 XX
 PS Claim 1; Columns 37-42; 32pp; English.
 XX
 CC Enterohaemorrhagic E.coli (EHEC) associated with enterohaemorrhagic
 CC colitis, haemolytic uremic syndrome and mesenteric adenitis have
 CC been found to carry a hlyA gene and a hlyB gene, separated by an
 CC intergenic region. The hly genes and the intergenic region are
 CC absent from bacteria not associated with these diseases and so
 CC provide a useful target for detecting EHEC pathogens, esp. O157:H7
 CC serotype E.coli. The present sequence is that of the protein
 CC encoded by the EHEC hlyA gene.
 XX
 SQ Sequence 758 AA;

Query Match 67.5%; Score 52; DB 17; Length 758;
 Best Local Similarity 57.1%; Pred. No. 1.4;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FNDIFHSGEGLDLL 14
 ||||| :|:|:
 Db 480 fndifhgadgndyi 493

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741 ggtctaataagtaaatgcaaaagctggcaatgacgatatcttgttgggtcaaggtaaaatg 1800
772 ggtctaataagtaaatgcaaaagctggcaatgacgatatcttgttgggtcaaggtaaaatg 2031
801 aatattgatgggtggagatggacacgacgtgtcttctatagtaagacggaggatttgggt 1860
832 aatattgatgggtggagatggacacgacgtgtcttctatagtaagacggaggatttgggt 2091
861 aatattactgtagatgggtacgagtgcaacagaagcaggcagttatacagttaatcgtaag 1920
892 aatattactgtagatgggtacgagtgcaacagaagcaggcagttatacagttaatcgtaag 2151
921 gttgctcgagggtgatattccatgaagttgtgaagcgtcaagaaccaagggtgggtaaa 1980
952 gttgctcgagggtgatattccatgaagttgtgaagcgtcaagaaccaagggtgggtaaa 2211
981 cgtactgaaactatccagtatcggtattgaattaaagaaaagttgggtatgggtatcag 2040
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1072 tctaccgataatttgaatcagtagaagaagtaattggttctcaatttaattgatgtattc 2331
1101 aaagggttctaaattcaacgacatattccatagtggtgaaggtgatgtatttactcgatggt 2160
1132 aaagggttctaaattcaacgacatattccatagtggtgaaggtgatgtatttactcgatggt 2391
1161 ggtgctggtgacgacgcgttgttttgggtggtaaaggcaacgacgactttctggagatgaa 2220
1192 ggtgctggtgacgacgcgttgttttgggtggtaaaggcaacgacgactttctggagatgaa 2451
1221 ggcgatgatttactcgatggcggttctggtgatgtattaaatgggtggtgctggtaat 2280
1252 ggcgatgatttactcgatggcggttctggtgatgtattaaatgggtggtgctggtaat 2511
1281 gatgtctatatcttctcgaaagggtgatggtaatgatactttgtacgatggcacgggcaat 2340
1312 gatgtctatatcttctcgaaagggtgatggtaatgatactttgtacgatggcacgggcaat 2571
1341 gataaattagcatttgcagatgcaaatatattctgatattatgattgaacgtaccaaaagag 2400
1372 gataaattagcatttgcagatgcaaatatattctgatattatgattgaacgtaccaaaagag 2631
1401 ggtattatagttaaacgaaatgatcattcaggtagtttaacataccaagatggttacata 2460
1432 ggtattatagttaaacgaaatgatcattcaggtagtttaacataccaagatggttacata 2691
1461 acatcaaatttacaattatcaaagtaataaaacagatcataaaattgagcaactaatt 2520
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1521 ggtaaagatggttagttatatcacttccgatcaaattgataaaattttgcaagataagaaa 2580
1552 ggtaaagatggttagttatatcacttccgatcaaattgataaaattttgcaagataagaaa 2811
1581 gatggtacagtaattacatctcaagaattgaaaaagcttgcgtgatgagaaataagagccaa 2640
1612 gatggtacagtaattacatctcaagaattgaaaaagcttgcgtgatgagaaataagagccaa 2871
1641 aaattatctgcttcggacattgcaagtagcttaataaagctagttgggtcaatggcacta 2700
1672 aaattatctgcttcggacattgcaagtagcttaataaagctagttgggtcaatggcacta 2931
1701 tttggtacagcaaatagtgtagttctaacgccttacagccaattacacaaccaactcaa 2760
1732 tttggtacagcaaatagtgtagttctaacgccttacagccaattacacaaccaactcaa 2991
1761 ggaattttgggtccaagtgttttag 2784
1992 ggaattttgggtccaagtgttttag 3015

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Qy 2540 tcacttcgacatacaattgataaaatttt 2567
1111 11 111 1111 111
Db 2528 tcacttcgacatacaattgataaaatttt 2555

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RESULT 2
 AAQ10727
 ID AAQ10727 standard; DNA; 2788 BP.
 XX
 AC AAQ10727;
 XX
 DT 11-APR-1991 (first entry)
 XX
 DE Leukotoxin 352 gene in plasmid PAA352.
 XX
 KW LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia;
 KW ds.
 XX
 OS Pasteurella haemolytica A1 strain B122.
 XX
 PN CA2014033-A.
 XX
 PD 07-OCT-1990.
 XX
 PF 06-APR-1990; 90CA-2014033.
 XX
 PR 07-APR-1989; 89US-0335018.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Acres SD, Babiuk LA, Potter AA, Lawman MJP;
 XX
 DR WPI; 1991-000097/01.
 DR P-PSDB; AAR10889.
 XX
 PT Pasteurella haemolytica proteins and genes - used for producing
 PT vaccines to protect animals esp. cattle from respiratory diseases
 PT e.g. pneumonia.
 XX
 PS Claim 13; Fig 5; 87pp; English.
 XX
 CC Plasmid PAA352 is derived from pAA114, a clone isolated from a
 CC genomic library of P. haemolytica. The protein encoded by the
 CC plasmid, "new leukotoxin" or "LKT 352" is 98% homologous to
 CC authentic leukotoxin. LKT 352 and pref. antigenic fragments of it,
 CC can be used in vaccines to protect cattle from respiratory diseases.
 CC They can also be used to produce antibodies for immunoaffinity
 CC purificn. of further proteins. [Fig. contg. sequence v. poor]
 CC See also AAR10890, AAR20909, AAR10910 and AAQ10783.
 XX
 SQ Sequence 2788 BP; 928 A; 487 C; 597 G; 776 T; 0 other;

Query Match 29.4%; Score 817.6; DB 12; Length 2788;
 Best Local Similarity 60.0%; Pred. No. 3.5e-171;
 Matches 1530; Conservative 0; Mismatches 964; Indels 54; Gaps 8;

Qy	53	caaagctcggattaaaaaatctttacttggctattccaaagattatgatccgcaaaaag	112
Db	29	caaaaactggggcaaaaaaattatcctctatattcccaaaattaccaatatgatactg	88
Qy	113	gtgggacttttaaatgattttattaaagctgctgatgaattaggtattgctcgtttagcag	172
Db	89	aacaaggtttacaggatttagtcaaagcggccgaagagttggggattgaggtacaaagag	148
Qy	173	aagagcctaatacactgaaacagcaaaaaaatctgttgacacagtaaatcagtttctct	232
Db	149	aagaacgcaataatattgcaacagctcaaacagtttaggcacgattcaaacgctattg	208
Qy	233	ctctcacacaaactggtattgctatttctgcaacaaaattagaaaagttcttacaaaaac	292
Db	209	gcttaactgagcgtggcattgtgttatccgctccacaaattgataaattgctacagaaa	267
Qy	293	attctaccaataagtttagccaaagggttagacagtgtagaaaaattgatcgtaaatag	352
Db	268	-----actaaagcaggccaagcattaggttctgcccgaagcattgtacaaaatgcaa	319
Qy	353	gtaaagcaagtaattgtattatcaacattaagctcttttttgggcactgcattagcgggta	412

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RESULT 9

AAR10889

ID AAR10889 standard; Protein; 924 AA.

XX

AC AAR10889;

XX

DT 11-APR-1991 (first entry)

XX

DE Leukotoxin 352 encoded by plasmid pAA352.

XX

KW LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia.

XX

OS Pasteurella haemolytica A1 strain B122.

XX

PN CA2014033-A.

XX

PD 07-OCT-1990.

XX

06-APR-1990; 90CA-2014033.

07-APR-1989; 89US-0335018.

UUSA-) UNIV SASKATCHEWAN.

Acres SD, Babiuk LA, Potter AA, Lawman MJP;

DR WPI; 1991-000097/01.

DR N-PSDB; AAQ10272.

XX

PT Pasteurella haemolytica proteins and genes - used for producing
PT vaccines to protect animals esp. cattle from respiratory diseases
PT e.g. pneumonia.

XX

PS Claim 13; Fig 5; 87pp; English.

XX

CC Plasmid pAA352 is derived from pAA114, a clone isolated from a
CC genomic library of P. haemolytica. The protein, designated "new
CC leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin.
CC LKT 352 and pref. antigenic fragments of it, can be used in
CC vaccines to protect cattle from respiratory diseases. They can also
CC be used to produce antibodies for immunoaffinity purification of
CC further proteins. [Fig. contg. sequence v. poor].
CC See also AAR10890, AAR10909, AAR10910 and AAQ10783.

XX

SQ Sequence 924 AA;

Query Match 63.6%; Score 49; DB 12; Length 924;
Best Local Similarity 58.3%; Pred. No. 5.7;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIFHSGEGDDL 13
||: | | :|||:
Db 745 ndllhggkgddi 756

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RESULT 1
B30169
leukotoxin A - Pasteurella haemolytica (serotype 1)
N:Alternate names: lktA protein
C:Species: Pasteurella haemolytica
C>Date: 12-Oct-1989 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C:Accession: B30169; C32051; S29516
R:Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.
DNA 8, 15-28, 1989
A>Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.
A:Reference number: A30169; MUID:89210283
A:Accession: B30169
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-953 <HIG>
R:Strathdee, C.A.; Lo, R.Y.C.
J. Bacteriol. 171, 916-928, 1989
A>Title: Cloning, nucleotide sequence, and characterization of genes encoding the
A:Reference number: A32051; MUID:89123172
A:Accession: C32051
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 947-953 <STR>
R:Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E.
Infect. Immun. 55, 1987-1996, 1987
A>Title: Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica A1
A:Reference number: S29515; MUID:87306837
A:Accession: S29516
A:Molecule type: DNA
A:Residues: 1-741, 'D', 743-953 <LOR>
A:Cross-references: EMBL:M20730; NID:g150492; PIDN:AAA25529.1; PID:g150494
C:Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
C:Genetics:
A:Gene: lktA
C:Function:
A:Description: lyses leukocytes
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem ;
F:238-784/Domain: hemolysin A homology <HLYA>
F:716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F:554/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 50.0%; Score 2325; DB 1; Length 953;
Best Local Similarity 49.9%; Pred. No. 1.6e-111;
Matches 464; Conservative 175; Mismatches 264; Indels 26; Gaps 13;

QY 8 KSNIQAGLNSTKSGKLNLYLAIPKD--YDPQGGTLDNFKADELGIARLAEEPNNHTET 65
Db 28 QSLTQAG-SSLKTGAKKIILYIPQNYQYDTEQGNGLQDLVKAEEELGIEVQREERNNIAT 86
QY 66 AKKSVDTVNFQSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLKASNVLS 125
Db 87 AQTSLGTIQTAGLTERGIVLSAPQIDKLLQK---TKAGQALGSAESIVQNANKAKTVLS 143
QY 126 TLSSFLGTALAGIELDSLIIKGDAPDALAKASIDLINEIIGNLSQSTOTIEAFSSQLAK 185
Db 144 GIQSILGSLVAGMDLDEAL-QNNSNOHALAKAGLELTNSLIENIANSVKTLDDEFGEQISQ 202
QY 186 LGSTISOAKGFSNIGNKLQNL-NFSKTNLGLLEIITGLLSGISAGFALADKNASTGKKVAA 244
Db 203 FGSKLQNIKGLGLTGLDKLKNIGGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVG 262
QY 245 GFELSNQVIGNVTKAISSYVLAQVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFN 304
Db 263 GFELANQVVGNIITKAVSSYILAQVAAGLSTTGVAALIASTVSLAISPLAFAGIADKFN 322
QY 305 HANALDEFKQFRKFGYDGDHLLAEYQRCVGTIEASLTITISTALGAVSAGVSAAGVSAV 364
Db 323 HAKSLESYAERFKKLGVDGDNLLAEYQRCGTGTIDASVTAINALAAIAGGVSAAGSVI 382
QY 365 GAPIALLVAGVTGLISGILEASKQAMPESVANRLQGKILEWEKQNGQNYFDKGYDSRYA 424
Db 383 ASPIALLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGNKYPENGVDARYL 442
QY 425 AYLANNLKFSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDG 484
Db 443 ANLQDNMKFLLNLNKLQAERVIAITQQQWDNNIGDLAGISRLGKVLGSKAYVDAFEEG 502
QY 485 KKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLK 544
Db 503 KHIKADKLVLQDSANGIIDVSNSGKAKTQHILFRTPLLTGTEHRERVOTGKYEYITKLN 562
QY 545 FGRVKNQVTDGEASSKLDPSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQ 597
Db 563 INRVDSWKITDGAASSTFDLTNNVQRIEGLDNAGNVTKTKETKIIAKLGEKDDNVFVGS 622
QY 598 GKMNIDGGDGHDRVFSYKDGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETK 657
Db 623 GTTEIDGGEYDRVHYSR-GNYGALTIDATKETEQQSYTVNRVETGKALHEVTSTHTAL 681
QY 658 VGKRTETIQRYDELKRVGYQSTDNLSVEEVIGSQFNDVFKGSKFNDIFHSGEKDD 717
Db 682 VGNREEKIEYR-HSNNQHAGYYTKDTLKAVEEIIIGTSHNDIFKGSKFNDAFNGGDDVDT 740
QY 718 LDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDDNDTLYDG 777
Db 741 IYGNDDNDRLFGGKGGDILDGGNGDDFIDGGKGNLHGGKGGDIFVHRKGGNDIITDS 800
QY 778 TGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRW----ITSNLQNYQSNKTD 833
Db 801 DGNKLSFSDSNLKDLTTFEKVKNLVI-TNSKKEKVTIQNWFEADFAKEVPNYKATK-D 858
QY 834 HKIEQLIGKDGSIYTSQDIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK 893
Db 859 EKIEEIQNGERITSKQVDDLI--AKGNKQITQDELSKVVDNYELLKHS-KNVTNSLOK 915

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